

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:32:04 : Search time 86.5 Seconds
(without alignments)
116.120 Million cell updates/sec

Title: US-10-608-584-1
28
Perfect score: 1 YMFVFLVFLGSPFLINLILAVVAVMAY 28
Sequence:

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_23Sep04:*

1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	447	7	ADB78592 Human sod
2	28	100.0	1381	5	AAE20513 Human ion
3	28	100.0	1387	5	AAE20514 Human ion
4	28	100.0	1392	5	AAE20518 Human ion
5	28	100.0	1398	5	AAE20519 Human ion
6	28	100.0	1442	5	AAE20512 Human ion
7	28	100.0	1453	5	AAE20517 Human ion
8	28	100.0	1795	7	ADB78596 Human sod
9	28	100.0	1855	7	ADB78597 Human sod
10	28	100.0	1962	5	AAE20511 Human ion
11	28	100.0	1973	5	AAE20516 Human ion
12	28	100.0	1981	7	ABR83185 Human SCN
13	28	100.0	1998	5	AAE20510 Human ion
14	28	100.0	1998	7	ABR83184 Human SCN
15	28	100.0	1999	5	ABR80626 Human sod
16	28	100.0	2005	4	AAE20516 Human ion
17	28	100.0	2005	4	AAE20516 Human ion
18	28	100.0	2005	5	ABR83627 Human GEF
19	28	100.0	2005	7	ADB78604 Human sod
20	28	100.0	2005	7	ADB78603 Human sod
21	28	100.0	2005	7	ADB78605 Human sod
22	28	100.0	2009	4	ADC46947 Human SCN
23	28	100.0	2009	5	AAE20515 Human ion
24	28	100.0	2009	5	ABG69292 Human sod

26	28	100.0	2009	5	ABG69291 Human sod
27	28	100.0	2009	5	ABG69293 Human sod
28	28	100.0	2009	5	ABG69289 Human sod
29	28	100.0	2009	5	ABG69290 Human sod
30	28	100.0	2009	5	ABR83626 Human GEF
31	28	100.0	2009	5	AAE16776 Human tra
32	28	100.0	2009	7	ADB78599 Human sod
33	28	100.0	2009	7	ADB78595 Human sod
34	28	100.0	2009	7	ADB78593 Human sod
35	28	100.0	2009	7	ADB78594 Human sod
36	28	100.0	2009	7	ADB78598 Human sod
37	28	100.0	2009	7	ABR83180 Human SCN
38	28	100.0	2009	7	ADP57563 Human pro
39	28	100.0	2009	7	ADP57561 Rat Prote
40	28	100.0	2009	2	AAE20516 Human ion
41	21	75.0	1977	2	AAE20516 Human ion
42	21	75.0	1977	8	ADP57702 Human pro
43	21	75.0	1978	7	ADP57563 Human pro
44	21	75.0	1978	7	ADP57563 Human pro
45	21	75.0	1978	7	ADP57563 Human pro
46	21	75.0	1984	2	AAE20516 Human ion
47	21	75.0	1984	2	AAE20516 Human ion
48	21	75.0	1984	7	ADP57561 Rat Prote
49	21	75.0	1984	7	ADP57561 Rat Prote
50	21	75.0	1989	2	AAE20516 Human ion
51	21	75.0	1989	2	AAE20516 Human ion
52	20	71.4	1836	7	ADP57388 Human pro
53	20	71.4	1836	7	ADP57388 Human pro
54	20	71.4	1836	7	ADP57388 Human pro
55	20	71.4	1836	8	ADP57388 Human pro
56	16	57.1	1024	5	ABR804858 Human sod
57	16	57.1	1950	7	ADB78607 Human sod
58	16	57.1	1951	4	AAE20516 Human ion
59	16	57.1	1951	4	AAE20516 Human ion
60	16	57.1	1951	7	ADP57388 Human pro
61	16	57.1	1951	8	ADP57388 Human pro
62	16	57.1	1951	8	ADP57388 Human pro
63	16	57.1	1956	4	AAE20516 Human ion
64	16	57.1	1956	4	AAE20516 Human ion
65	16	57.1	1956	6	ABG75945 Human per
66	16	57.1	1956	6	ABG75945 Human per
67	16	57.1	1956	6	ABG75945 Human per
68	16	57.1	1956	6	ABG75945 Human per
69	16	57.1	1956	8	ADP57388 Human pro
70	16	57.1	2000	5	ABR806027 Human sod
71	16	57.1	2000	8	ADP57388 Human pro
72	15	53.6	130	5	ADP57388 Human pro
73	14	50.0	1366	8	ADP57388 Human pro
74	14	50.0	1366	8	ADP57388 Human pro
75	13	46.4	1956	4	AAE20516 Human ion
76	13	46.4	1956	4	AAE20516 Human ion
77	13	46.4	1956	6	ABG75944 Human per
78	13	46.4	1956	6	ADP57388 Human pro
79	13	46.4	1956	6	ADP57388 Human pro
80	13	46.4	1957	2	AAE20516 Human ion
81	13	46.4	1957	2	AAE20516 Human ion
82	13	46.4	1957	6	ABG75945 Human per
83	13	46.4	1957	6	ABG75945 Human per
84	13	46.4	1957	6	ADP57388 Human pro
85	13	46.4	1957	7	ADP57388 Human pro
86	13	46.4	1957	8	ADP57388 Human pro
87	13	46.4	1958	4	AAE20516 Human ion
88	13	46.4	1962	4	AAE20516 Human ion
89	13	46.4	2132	2	AAE20516 Human ion
90	12	42.9	1234	5	AAE20516 Human ion
91	12	42.9	1234	5	AAE20516 Human ion
92	12	42.9	1243	2	AAE20516 Human ion
93	12	42.9	1243	4	AAE20516 Human ion
94	12	42.9	1444	5	AAO14926 Human sod
95	12	42.9	1791	4	AAO14925 Human sod
96	12	42.9	1791	5	AAO14925 Human sod
97	12	42.9	1791	7	ADP57388 Human pro
98	11	39.3	442	4	ABG04326 Human sod

99 11 39.3 1107 6 ABR41495
100 11 39.3 1603 4 AAU19518

Abi-41495 Human DIT
AAU19518 Human dia

ALIGNMENTS

RESULT 1
ADB78592

ID ADB78592 standard; protein; 447 AA.

XX ADB78592;

DT 04-DEC-2003 (first entry)

DE Human sodium channel subunit mutant SEQ ID NO:136.

XX KW mutin; mutant; ion channel; ion channel subunit; ICS; neurotropic;
KW neuroprotective; inotropic; antidiabetic; antihypertensive; antidiabetic;
KW nephroprotective; antidiabetic; antihypertensive; antidiabetic; antidiabetic;
KW ion channel dysfunction; human.

XX OS Synthetic.

XX OS Homo sapiens.

PN MO2003008574-A1.

PD 30-JAN-2003.

PF 08-JUL-2002; 2002MO-AU000910.

PR 18-JUL-2001; 2001AU-00006452.

PR 05-MAR-2002; 2002AU-00000910.

PR 13-MAY-2002; 2002AU-00002292.

PA (BION-) BIONOMICS LTD.

PA (WALL/) WALLACE R W.

PI Mulvey JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;

DR WPI; 2003-239332/23.

XX N-PSDB; ADB78631.

PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
XX mutation events.

PS Claim 13; SEQ ID NO 136; 106pp; English.

XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has neurotropic, neuroprotective, inotropic, antidiabetic,
XX antihypertensive, antidiabetic, antidepressant, antiparkinsonian,
XX neuroleptic, tranquilizer, analgesic, nephroprotective, antidiabetic,
XX ophthalmological activity. A polynucleotide of the invention acts as an
XX ion channel agonist, or ion channel antagonist. The methods, isolated
XX nucleic acids, polypeptides, antibody, selective agonist, antagonist or
XX modulator of an ion channel, cells and genetically modified non-human
XX animal, are useful for the diagnosis and treatment of epilepsy and/or a
XX disorder associated with ion channel dysfunction, such as hyper- or hypo-
XX kalemia, periodic paralysis, myotonia, malignant hyperthermia,
XX disease, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
XX depression, phobic obsessive symptoms, neuropathic pain, inflammatory
XX pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
XX Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
XX fibrosis, congenital stationary night blindness and total colour

CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX SQ Sequence 447 AA;

Query Match 100.0%; Score 28; DB 7; Length 447;
Best Local Similarity 100.0%; Pred. No. 5.4e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMIFVTVFLGSPFLINILAVVAVAY 28
Db 399 YMIFVTVFLGSPFLINILAVVAVAY 426

RESULT 2

AAE20513

ID AAE20513 standard; protein; 1381 AA.

XX AAE20513;

DT 01-JUL-2002 (first entry)

DE Human ion channel protein #4.

XX KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
XX medical disorder.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FT MISC-difference 981 /note= "Encoded by MTG"

FT MISC-difference 1056 /note= "Encoded by RCA"

PN MO200214498-A2.

XX 21-FEB-2002.

PF 15-AUG-2001; 2001MO-US025650.

PR 16-AUG-2000; 2000US-0225989P.

PA (LEXI-) LEXICON GENETICS INC.

PI Turner CA, Mathur B, Mathur D;

PI WPI; 2002-280757/32.

DR N-PSDB; AAD32842.

XX Novel polynucleotides encoding human sodium channel proteins,
XX particularly voltage-gated sodium channel proteins useful for drug
XX screening, diagnosis and in gene therapy of biological disorders.

PS Claim 1; Page 47-50; 83pp; English.

XX The present sequence is novel human protein (NHP), ion channel protein.
XX NHP share structural similarity with mammalian sodium channel proteins.
XX particularly voltage-gated sodium channel proteins. NHP oligonucleotides
XX are useful as hybridization probes for screening libraries and assessing
XX gene expression patterns. Sequences derived from regions adjacent to the
XX intron/exon boundaries of NHP gene can be used to design primers for use
XX in amplification assays to detect mutations within the exons, splice
XX sites, introns that can be used in diagnostics and pharmacogenomics. NHP
XX nucleotide sequences are useful for drug screening effective in the
XX treatment of symptomatic or phenotypic manifestations of perturbing the
XX normal function of NHP in the body, and nucleotide constructs encoding the
XX NHP products are useful to genetically engineer host cells to express NHP
XX products in vivo. These genetically engineered cells function as
XX bioreactors in the body delivering a continuous supply of a NHP, a NHP

peptide, or a NHP fusion protein to the body. Nucleotide construct encoding NHP products are also useful in gene therapy for modulating NHP expression and to produce genetically engineered host cells to express NHP products in vivo. NHP nucleotide sequences may also be used as part of ribozyme and/or triple helix sequences that are useful for NHP gene regulation. The NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases

Sequence 1381 AA;

Query Match 100.0%; Score 28; DB 5; Length 1381;
Best Local Similarity 100.0%; Pred. No. 1.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMFFVLVIFLGSPYLINILIAVVMAY 28
|||
Db 399 YMFFVLVIFLGSPYLINILIAVVMAY 426

RESULT 3
AAE20514
ID AAE20514 standard; protein; 1387 AA.
XX
AC AAE20514;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #5.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FH Misc-difference 981
FT /note= "Encoded by MTG"
FT Misc-difference 1056
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR MPI; 2002-280757/32.
DR N-PSDB; AAD32843.
XX

Novel polynucleotides encoding human sodium channel proteins, particularly voltage-gated sodium channel proteins useful for drug screening, diagnosis and in gene therapy of biological disorders.

Claim 1; Page 52-55; 83pp; English.

The present sequence is novel human protein (NHP), ion channel protein. NHP share structural similarity with mammalian sodium channel proteins particularly voltage-gated sodium channel proteins. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene expression patterns. Sequences derived from regions adjacent to the intron/exon boundaries of NHP gene can be used to design primers for use in amplification assays to detect mutations within the exons, splice sites, introns that can be used in diagnostics and pharmacogenomics. NHP

nucleotide sequences are useful for drug screening effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body, and nucleotide constructs encoding NHP products are useful to genetically engineer host cells to express NHP products in vivo. These genetically engineered cells function as bioreactors in the body delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide construct encoding NHP products are also useful in gene therapy for modulating NHP expression and to produce genetically engineered host cells to express NHP products in vivo. NHP nucleotide sequences may also be used as part of ribozyme and/or triple helix sequences that are useful for NHP gene regulation. The NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases

Sequence 1387 AA;

Query Match 100.0%; Score 28; DB 5; Length 1387;
Best Local Similarity 100.0%; Pred. No. 1.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMFFVLVIFLGSPYLINILIAVVMAY 28
|||
Db 399 YMFFVLVIFLGSPYLINILIAVVMAY 426

RESULT 4
AAE20518
ID AAE20518 standard; protein; 1392 AA.
XX
AC AAE20518;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #9.
XX
KW Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioreactor; mental disorder; biological disorder;
KW medical disorder.
XX
OS Homo sapiens.
XX

Key Location/Qualifiers
FH Misc-difference 992
FT /note= "Encoded by MTG"
FT Misc-difference 1067
FT /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR MPI; 2002-280757/32.
DR N-PSDB; AAD32847.
XX

Novel polynucleotides encoding human sodium channel proteins, particularly voltage-gated sodium channel proteins useful for drug screening, diagnosis and in gene therapy of biological disorders.

Claim 1; Page 75-78; 83pp; English.

The present sequence is novel human protein (NHP), ion channel protein. NHP share structural similarity with mammalian sodium channel proteins

RESULT 5	
AAE20519	
ID	AAE20519
XX	standard; protein; 1398 AA.

Human ion channel protein #10.

Homo sapiens.

```

/note= "Encoded by MTG"
1007
MiBC-difference

```

/note= "Encoded by RCA"

WO200214498-A2.

21-FEB-2002.

15-AUG-2001; 2001WO-US025650.

16-AUG-2000; 2000US-0225989P.

(LEXI-) LEXICON GENETICS INC.

Turner CA, Mathur B, Mathur D;

WPI; 2002-280757/32.
N-PSDB: 77522243

Novel polyaniline...

novel polynucleotides encoding human sodium channel proteins, particularly voltage-gated sodium channel proteins useful for drug

The present sequence is novel human protein (NHP), ion channel protein. NHP share structural similarity with mammalian sodium channel proteins. Particularly voltage-gated sodium channel proteins. NHP oligonucleotides are useful as hybridisation probes for screening libraries and assessing gene expression patterns. Sequences derived from regions adjacent to the intron/exon boundaries of NHP gene can be used to design primers for use in amplification assays to detect mutations within the exons, splice sites, introns that can be used in diagnostics and pharmacogenomics. NHP nucleotide sequences are useful for drug screening effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body, and nucleotide constructs encoding the NHP products are useful to genetically engineer host cells to express NHP products in vivo. These genetically engineered cells function as bioreactors in the body delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. Nucleotide construct encoding NHP products are also useful in gene therapy for modulating NHP expression and to produce genetically engineered host cells to express NHP products in vivo. NHP nucleotide sequences may also be used as part of ribozyme and/or triple helix sequences that are useful for NHP gene regulation. The NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases

[illegible]

RESULT 6	
AAE20512	
ID	AAE20512 standard; protein; 1442 AA
XX	

AC	AAE20512;
XX	
DT	01-JUL-2002 (first entry)
XX	

Human ion channel protein #3.

Human; novel human protein; NHP; voltage-gated sodium channel; gene therapy; bioreactor; mental disorder; biological disorder; medical disorder.

Homo sapiens.

Key	Location/Qualifiers
EH	
Key	
vi	
...	

```

1000  REFERENCE 501
1001  /notes= "Encoded by MTC"
1002  v1= 31.5
1003  PFT
1004  END

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1056 /note= "Encoded by RCA"

WO200214498-A2.

21-FEB-2002.

15-AUG-2001; 2001WO-US025650.

16-AUG-2000; 2000US-0225989P.

(LEXI-) LEXICON GENETICS INC.

I Turner CA, Mathur B, Mathur D;

XX WPI; 2002-280757/32.
DR N-PSDB; AAD32841.
XX
XX Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1, Page 43-46; 83pp; English.

XX The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or tripe helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases

XX Sequence 1442 AA;
SQ

Query Match 100.0%; Score 28; DB 5; Length 1442;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMIFFVLVIPLGSGFYLNILILAVVAMAY 28
DB 399 YMIFFVLVIPLGSGFYLNILILAVVAMAY 426

RESULT 7
ID AAE20517 standard; protein; 1453 AA.
XX
XX AAE20517;
XX
XX 01-JUL-2002 (first entry)
XX
XX Human ion channel protein #8.
XX
XX Human, novel human protein; NHP; voltage-gated sodium channel;
XX gene therapy; bioreactor; mental disorder; biological disorder;
XX medical disorder.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 992 /note= "Encoded by MTG"
XX FT Misc-difference 1067 /note= "Encoded by RCA"
XX FT
XX WO200214498-A2.
XX PN
XX 21-FEB-2002.
XX PD
XX 15-AUG-2001; 2001WO-US025650.
XX PF

XX 16-AUG-2000; 2000US-0225989P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Mathur D;
XX
XX WPI; 2002-280757/32.
XX N-PSDB; AAD32846.
XX
XX Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1, Page 70-73; 83pp; English.

XX The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or tripe helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases

XX Sequence 1453 AA;
SQ

Query Match 100.0%; Score 28; DB 5; Length 1453;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMIFFVLVIPLGSGFYLNILILAVVAMAY 28
DB 399 YMIFFVLVIPLGSGFYLNILILAVVAMAY 426

RESULT 8
ID ADB78596 standard; protein; 1795 AA.
XX
XX ADB78596;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human sodium channel subunit mutant SEQ ID NO:140.
XX
XX Human, mutant; ion channel; ion channel subunit; ICS; nootropic;
XX neuroprotective; inotropic; antiparkinsonian; neuroleptic; analgesic;
XX antidiabetic; ophthalmological; epilepsy;
XX ion channel dysfunction; human.
XX
XX Synthetic.
XX Homo sapiens.
XX WO2003008574-A1.
XX PN
XX

PD 30-JAN-2003.
 XX
 PF 08-JUL-2002; 2002MO-AU000910.
 XX
 PR 18-JUL-2001; 2001AU-00006452.
 PR 05-MAR-2002; 2002AU-00000910.
 PR 13-MAY-2002; 2002AU-00002292.
 XX
 PA (BION-) BIONOMICS LTD.
 PA (WALL/) WALLACE R W.
 PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE,
 PI Berkovic SF, Scheffer IE;
 XX
 DR WPI: 2003-239332/23.
 DR N-PSDB; ADB78635.
 XX
 PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 140; 106pp; English.
 XX
 CC The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
 CC antirhythmic, antigraine, antidepressant, antiparkinsonian,
 CC analgesic, anxiolytic, antipruritic, antidiabetic, and
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemia, periodic paralysis, myotonia, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, hyperphagia, anxiety,
 CC depression, Parkinson's disease, schizophrenia, hyperphagia, anxiety,
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 CC
 SQ Sequence 1795 AA;
 Query Match 100.0%; Score 28; DB 7; Length 1795;
 Best Local Similarity 100.0%; Pred. No. 1.7e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YMFVFLVIFGSGFYLNILAVVAMAY 28
 Db 399 YMFVFLVIFGSGFYLNILAVVAMAY 426
 RESULT 9
 ID ADB78597
 XX ADB78597 standard; protein; 1855 AA.
 AC ADB78597;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human sodium channel subunit mutant SEQ ID NO:141.
 XX
 KW mutein, mutant; ion channel; ion channel subunit; ICS; nootropic;
 KW neuroprotective; inotropic; antipyretic; antirhythmic; antigraine;

KW antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;
 KW neuroprotective; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PW WO2003008574-A1.
 XX
 FD 30-JAN-2003.
 XX
 PF 08-JUL-2002; 2002MO-AU000910.
 XX
 PR 18-JUL-2001; 2001AU-00006452.
 PR 05-MAR-2002; 2002AU-00000910.
 PR 13-MAY-2002; 2002AU-00002292.
 XX
 PA (BION-) BIONOMICS LTD.
 PA (WALL/) WALLACE R W.
 PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE,
 PI Berkovic SF, Scheffer IE;
 XX
 DR WPI: 2003-239332/23.
 DR N-PSDB; ADB78636.
 XX
 PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 141; 106pp; English.
 XX
 CC The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
 CC antirhythmic, antigraine, antidepressant, antiparkinsonian,
 CC analgesic, anxiolytic, antipruritic, antidiabetic, and
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemia, periodic paralysis, myotonia, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, hyperphagia, anxiety,
 CC depression, Parkinson's disease, schizophrenia, hyperphagia, anxiety,
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 CC
 SQ Sequence 1855 AA;
 Query Match 100.0%; Score 28; DB 7; Length 1855;
 Best Local Similarity 100.0%; Pred. No. 1.8e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YMFVFLVIFGSGFYLNILAVVAMAY 28
 Db 399 YMFVFLVIFGSGFYLNILAVVAMAY 426
 RESULT 10
 ID AAE20511
 XX AAE20511 standard; protein; 1962 AA.

XX AAE20511;
AC
XX 01-JUL-2002 (first entry)
DT
XX Human ion channel protein #2.
DE
XX Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioresactor; mental disorder; biological disorder;
KW medical disorder.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 981 /note= "Encoded by MTG"
FT Misc-difference 1056 /note= "Encoded by RCA"
FT
XX MO20021498-AZ.
XX
XX 21-FEB-2002.
XX
XX 15-AUG-2001; 2001WO-US025650.
XX
XX 16-AUG-2000; 2000US-0225989P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Mathur D;
XX
XX MPI; 2002-280757/32.
DR N-PSDB; AAD32840.
XX
XX Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
XX Claim 1; Page 37-41; 83pp; English.

XX The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding the
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioresactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or tripe helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
XX Sequence 1962 AA;
SQ

Query Match 100.0%; Score 28; DB 5; Length 1962;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YMIFFVLVIFLGsfYILNLLAVVAMAY 28
|||||

DB 399 YMIFFVLVIFLGsfYILNLLAVVAMAY 426

RESULT 11
AAE20516
ID AAE20516 standard; protein; 1973 AA.
XX
XX AAE20516;
AC
XX 01-JUL-2002 (first entry)
DT
XX Human ion channel protein #7.
DE
XX Human; novel human protein; NHP; voltage-gated sodium channel;
KW gene therapy; bioresactor; mental disorder; biological disorder;
KW medical disorder.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 992 /note= "Encoded by MTG"
FT Misc-difference 1067 /note= "Encoded by RCA"
FT
XX MO20021498-AZ.
XX
XX 21-FEB-2002.
XX
XX 15-AUG-2001; 2001WO-US025650.
XX
XX 16-AUG-2000; 2000US-0225989P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Turner CA, Mathur B, Mathur D;
XX
XX MPI; 2002-280757/32.
DR N-PSDB; AAD32845.
XX
XX Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
XX Claim 1; Page 64-68; 83pp; English.

XX The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the
CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding the
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioresactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or tripe helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
XX Sequence 1973 AA;
SQ

Db	399	YMIFFVLVIFLGSPFLINILIAVVMAY	426
		RESULT 14	
XX	ID	ABR83184	standard; protein; 1998 AA.
XX	AC	ABR83184;	
XX	DT	15-JAN-2004	(first entry)
XX	DE	Human SCN1A splice variant -33p:SCN1ADel671-681.	
XX	KW	SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;	
XX	KM	neuroprotective; anesthetic; cytosolic; cerebroprotective; cardiac;	
XX	XX	hypotensive; gene therapy; human; splice variant.	
OS		Homo sapiens.	
PN		WO2003072751-A2.	
PD		04-SEP-2003.	
XX	PF	25-FEB-2003; 2003WO-US006010.	
XX	PR	25-FEB-2002; 2002US-0359382P.	
XX	PA	(UYVA-) UNIV VANDERBILT.	
XX	PI	George AL, Lossin C;	
XX	DR	WPI; 2003-712725/67.	
XX	DR	N-PSDB; ACF57879.	
PT		Recombinantly expressed sodium channel type 1 alpha subunit, useful in	
XX	XX	screening for modulators, for treating e.g. epilepsy.	
XX	XX	Disclosure; Page 148-156; 176pp; English.	
CC		The invention relates to a recombinantly expressed and isolated human	
CC		SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally	
CC		incorporated into a cell, is used to screen for specific modulators,	
CC		potentially useful as anticonvulsant, antiepileptic, neuroprotective,	
CC		analgesic and/or anesthetic agents, e.g. for treating severe myoclonic	
CC		epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,	
CC		motor endplate diseases, hypertension, congestive heart failure and	
CC		muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic	
CC		and metastatic cancer cell lines). These activities can also be provided	
CC		by gene therapy vectors that express (I) or the modulators. The	
CC		modulator, also antibodies directed against (I), are used to detect	
CC		sodium channel polypeptides. The present sequence represents a human	
CC		SCN1A splice variant 33p:SCN1ADel671-681 encoding cDNA	
SO		Sequence 1998 AA;	
OY		Query Match 100.0%; Score 28; DB 7; Length 1998;	
Db		Best Local Similarity 100.0%; Pred. No. 1.9e-18;	
		Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
		1 YMIFFVLVIFLGSPFLINILIAVVMAY 28	
		399 YMIFFVLVIFLGSPFLINILIAVVMAY 426	
RESULT 15			
ABR06026			
ID		ABR06026 standard; protein; 1999 AA.	
XX	AC	ABR06026;	
XX	DT	10-MAY-2002	(first entry)
XX	DE	Human sodium channel SCN1A protein SEQ ID NO:2.	

KW	Human; sodium channel; SCN1A; chromosome 2q24;
KM	familial hypercalcaemic periodic paralysis; motor enplate disease.
XX	
OS	Homo sapiens.
PX	
XX	WO200196552-A1.
XX	
PD	20-DEC-2001.
XX	
PF	12-JUN-2001; 2001WO-JP004956.
XX	
PR	13-JUN-2000; 2000JP-00177540.
PR	13-JUN-2000; 2000JP-00177544.
XX	
PA	(NISC-) JAPAN SCI & TECHNOLOGY CORP.
PI	
PI	Kanazawa I, Goto J, Jeong S;
XX	
DR	WPt; 2002-098066/13.
DR	N-PsDB; ABL39689.
PT	
XX	Human sodium channels SCN1A and SCN3A and encoded genes, useful in studying physiological mechanism in which excitant cells participate and causes of diseases and developing drugs for motor enplate disease. Claim 1; Page 40-49; 88pp; Japanese.
PS	
XX	The present invention describes human sodium channels SCN1A and SCN3A. The present sequence represents the human sodium channel SCN1A. SCN1A and SCN3A have been located to the human chromosome 2 long arm, positions 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in studying the physiological mechanism in which excitant cells participate and cause human diseases, and in developing remedies for e.g. familial hypercalcaemic periodic paralysis of extremities and motor enplate disease
CC	
CC	
XX	Sequence 1999 AA:
SQ	
Query Match	100.0%; Score 28; DB 5; Length 1999;
Best Local Similarity	100.0%; Pred. No. 1,9e-18;
Matches	28; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 YMIFFVLVIAGSFYLINLIIVAVVAMAY 28
Dn	399 YMIFFLVIFGSEFYLINLIIVAVVAMAY 426
RESULT 16	
AAB99676	
ID	AAB99676 standard; protein; 2005 AA.
XX	
AC	AAB99676;
XX	
DT	04-SEP-2001 (first entry)
DE	
XX	Human adult form of SCN2A protein sequence SEQ ID NO:35.
XX	
KW	Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification; diagnosis; mutation; chromosome 2q23-q31; neurological disorder; anticonvulsant; neuroprotective.
KM	
XX	
OS	Homo sapiens.
XX	
PN	WO200138564-A2.
XX	
PD	31-MAY-2001.
XX	
PF	24-NOV-2000; 2000WO-CA001404.
XX	
PR	26-NOV-1999; 99US-0167623P.
XX	
PA	(UTMC-) UNIV MCGILL.

XX Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
 XX WPI, 2001-355945/37.
 DR N-PSDB; AAH55793.
 XX
 PT Determining a predisposition to epilepsy and/or development of epilepsy
 PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
 XX variant, equivalent, or mutation which shows a linkage disequilibrium.
 XX Disclosure; Page 123-130; 268pp; English.
 CC The present invention describes a method (M1) of determining an
 CC individual's predisposition to epilepsy and/or development of epilepsy,
 CC as well as predicting the individual's response to medication. The method
 CC comprises determining the genotype of at least one gene selected from
 CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
 CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
 CC channel genes located on chromosome 2. The idiopathic generalised
 CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
 CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
 CC or other neurological disorders. They have anticonvulsant and
 CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
 CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
 CC oligonucleotides and proteins given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 2005 AA;
 Query Match 100.0%; Score 28; DB 4; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 YMIFVLVIFLGSFYILNILLAVVMAY 28
 DB 401 YMIFVLVIFLGSFYILNILLAVVMAY 428
 RESULT 17
 AAB99677
 ID AAB99677 standard; protein, 2005 AA.
 AC AAB99677;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human neonatal form of SCN2A protein sequence SEQ ID NO:36.
 XX
 KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
 KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
 KW anticonvulsant; neuroprotective.
 OS Homo sapiens.
 XX
 PN W0200138564-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 24-NOV-2000; 2000WO-CA001404.
 XX
 PR 26-NOV-1999; 99US-0167623P.
 XX
 PA (UMC-) UNITV MCGILL.
 XX
 PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
 XX WPI, 2001-355945/37.
 DR N-PSDB; AAH55794.
 XX
 PT Determining a predisposition to epilepsy and/or development of epilepsy
 PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
 XX variant, equivalent, or mutation which shows a linkage disequilibrium.
 XX Disclosure; Page 123-130; 268pp; English.

XX Disclosure; Page 131-138; 268pp; English.
 XX
 PS The present invention describes a method (M1) of determining an
 CC individual's predisposition to epilepsy and/or development of epilepsy,
 CC as well as predicting the individual's response to medication. The method
 CC comprises determining the genotype of at least one gene selected from
 CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
 CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
 CC channel genes located on chromosome 2. The idiopathic generalised
 CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
 CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
 CC or other neurological disorders. They have anticonvulsant and
 CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
 CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
 CC oligonucleotides and proteins given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 2005 AA;
 Query Match 100.0%; Score 28; DB 4; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 YMIFVLVIFLGSFYILNILLAVVMAY 28
 DB 401 YMIFVLVIFLGSFYILNILLAVVMAY 428
 RESULT 18
 ABB83627
 ID ABB83627 standard; protein, 2005 AA.
 AC ABB83627;
 XX
 DT 10-OCT-2002 (first entry)
 XX
 DE Human GEFs+ protein with SCN2A mutation.
 XX
 KW Human; GEFs+; SCN2A; mutant; mutein;
 KW generalized epilepsy with febrile seizure plus.
 OS Homo sapiens.
 XX
 PN JP2002136289-A.
 XX
 PD 14-MAY-2002.
 XX
 PF 01-NOV-2000; 2000JP-00334969.
 XX
 PR 01-NOV-2000; 2000JP-00334969.
 XX
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
 PA (RIKA) RIKAGAKU KENKYUSHO.
 XX
 PI WPI: 2002-552308/59.
 DR N-PSDB; ABO79201.
 XX
 PT A human polynucleotide which is complementary to an mRNA transcribed from
 PT useful for diagnosing GEFs+.
 XX
 PS Claim 10; Page 29-34; 37pp; Japanese.
 CC This invention relates to a human polynucleotide which is complementary
 CC to an mRNA transcribed from a "generalized epilepsy with febrile seizure
 CC plus" (GEFS+)-related gene. The gene is useful for diagnosing GEFs+. The
 CC present sequence represents the human GEFs+ protein sequence with SCN2A
 CC mutation
 XX
 SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 5; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YMIFFVLVIFLGSFYILNIIILAVVMAY 28
 |||||
 DB 401 YMIFFVLVIFLGSFYILNIIILAVVMAY 428

RESULT 19
 ADB78604
 ID ADB78604 standard; protein; 2005 AA.
 XX
 AC ADB78604;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human sodium channel subunit mutant SEQ ID NO:148.
 XX
 KM mutein; mutant; ion channel; ion channel subunit; ICS; noctropic;
 KM neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KM antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KM nephrotropic; antidiabetic; ophthalmological; epilepsy;
 KM ion channel dysfunction; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO2003008574-A1.
 XX
 PD 30-JAN-2003.
 XX
 PE 08-JUL-2002; 2002WO-AU000910.
 XX
 PR 18-JUL-2001; 2001AU-00006452.
 PR 05-MAR-2002; 2002AU-0000910.
 PR 13-MAY-2002; 2002AU-00002292.
 XX
 PA (BION-) BIONOMICS LTD.
 PA (WALL/) WALLACE R W.
 XX
 PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
 PI Berkovic SF, Scheffer IE;
 XX
 DR WPI: 2003-239332/23.
 DR N-PSDB: ADB78643.
 XX
 PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 148; 106pp; English.
 XX
 CC The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has noctropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antidiabetic, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonia, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,

CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 CC
 XX

SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YMIFFVLVIFLGSFYILNIIILAVVMAY 28
 |||||
 DB 401 YMIFFVLVIFLGSFYILNIIILAVVMAY 428

RESULT 20
 ADB78603
 ID ADB78603 standard; protein; 2005 AA.
 XX
 AC ADB78603;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human sodium channel subunit mutant SEQ ID NO:147.
 XX
 KM mutein; mutant; ion channel; ion channel subunit; ICS; noctropic;
 KM neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KM antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KM nephrotropic; antidiabetic; ophthalmological; epilepsy;
 KM ion channel dysfunction; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FN WO2003008574-A1.
 XX
 PD 30-JAN-2003.
 XX
 PE 08-JUL-2002; 2002WO-AU000910.
 XX
 PR 18-JUL-2001; 2001AU-00006452.
 PR 05-MAR-2002; 2002AU-0000910.
 PR 13-MAY-2002; 2002AU-00002292.
 XX
 PA (BION-) BIONOMICS LTD.
 PA (WALL/) WALLACE R W.
 XX
 PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
 PI Berkovic SF, Scheffer IE;
 XX
 DR WPI: 2003-239332/23.
 DR N-PSDB: ADB78642.
 XX
 PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 147; 106pp; English.
 XX
 CC The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has noctropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antidiabetic, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated

CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonia, malignant hyperthermia, or hypo-
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WFO at ftp.wipo.int/pub/published_pat_sequences.

SO Sequence 2005 AA;
 Query Match 100.0%; Score 28; DB 7; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YMFVFLVFLGSPYLINILAVVAMAY 28
 DB 401 YMFVFLVFLGSPYLINILAVVAMAY 428

RESULT 21
 ADB78605
 ID ADB78605 standard; protein; 2005 AA.
 XX ADB78605;
 XX
 DT 04-DEC-2003 (first entry)
 DE Human sodium channel subunit mutant SEQ ID NO:149.
 XX

KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
 KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.

XX Synthetic.
 OS Homo sapiens.
 PN WO2003008574-A1.
 PD 30-JAN-2003.
 PF 08-JUL-2002; 2002WO-AU000910.
 PR 18-JUL-2001; 2001AU-00006452.
 PR 05-MAR-2002; 2002AU-0000910.
 PR 13-MAY-2002; 2002AU-00002292.

PA (BION-) BIONOMICS LTD.
 PA (WALL-) WALLACE R W.

PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE,
 PI Berkovic SF, Scheffer IE;
 DR WPI; 2003-239332/23.
 DR N-PSDB; ADB78644.

PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.

PS Claim 13; SEQ ID NO 149; 106pp; English.

XX The invention relates to a novel method for identifying a subject

CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonia, malignant hyperthermia, or hypo-
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WFO at ftp.wipo.int/pub/published_pat_sequences.

SO Sequence 2005 AA;
 Query Match 100.0%; Score 28; DB 7; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 1.9e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YMFVFLVFLGSPYLINILAVVAMAY 28
 DB 401 YMFVFLVFLGSPYLINILAVVAMAY 428

RESULT 22
 ADC46947
 ID ADC46947 standard; protein; 2005 AA.
 XX ADC46947;
 XX
 DT 18-DEC-2003 (first entry)
 DE Human SCN2A amino acid sequence #SEQ ID 3.
 XX

KW SCN2A; voltage-gated ion channel; human; neuroprotective; gene therapy;
 KW vaccine; Alzheimer's disease.
 KW Homo sapiens.
 OS
 PN WO2003060525-A1.
 PD 24-JUL-2003.
 PF 16-JAN-2003; 2003WO-EP000400.
 PR 17-JAN-2002; 2002EP-00001236.
 PR 17-JAN-2002; 2002US-0348674P.

PA (EVOT-) EVOTEC NEUROSCIENCES GMBH.
 PA
 PI Hipfel R, Von Der Kammer H, Pohlner J;
 PI
 DR WPI; 2003-598580/56.
 DR N-PSDB; ADC46961.

PT Diagnosing or prognosticating a neurodegenerative disease by detecting
 PT the level or activity of transcription or translation products of the
 PT gene coding for the voltage-gated ion channel SCN2A.
 PS Disclosure; Fig 9; 67pp; English.

CC The invention relates to a method for diagnosing or prognosticating a
CC neurodegenerative disease in a subject, or determining whether a subject
CC is at increased risk of developing the disease. The method comprises
CC detecting the level and/or activity of a transcription or translation
CC product of the gene coding for the voltage-gated ion channel SCN2A. The
CC modulator of an activity and/or of a level of at least one substate is
CC useful for preparing a composition for treating or preventing a
CC neurodegenerative disease, in particular Alzheimer's disease. The current
CC sequence represents the human SCN2A amino acid sequence.

XX
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YMFFVLVIFLGSPFLINILAVVMAY 28
|||
DB 401 YMFFVLVIFLGSPFLINILAVVMAY 428

RESULT 23

AAB99674 ID AAB99674 standard; protein; 2009 AA.

XX AAB99674;

DT 04-SEP-2001 (first entry)

DE Human adult form of SCN1A protein sequence SEQ ID NO:3.

XX Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;

KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;

KW anticonvulsant; neuroprotective.

XX Homo sapiens.

OS WO200138564-A2.

PN 31-MAY-2001.

XX 24-NOV-2000; 2000WO-CA001404.

XX 26-NOV-1999; 99US-0167623P.

XX (UMC-) UNIV MCGILL.

XX Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;

DR MPI; 2001-355945/37.

XX N-PSDB; AAH55763.

PT Determining a predisposition to epilepsy and/or development of epilepsy

PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA

PT variant, equivalent, or mutation which shows a linkage disequilibrium.

XX Disclosure: Page 96-104; 268pp; English.

XX The present invention describes a method (M1) of determining an

XX individual's predisposition to epilepsy and/or development of epilepsy,

XX as well as predicting the individual's response to medication. The method

XX comprises determining the genotype of at least one gene selected from

XX SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which

XX shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium

XX channel genes located on chromosome 2. The idiopathic generalised

XX epilepsy (IGE) gene is more specifically localised on chromosome 2q23-

XX q31. Compounds identified as modulators of the biological activity of

XX SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy

XX or other neurological disorders. They have anticonvulsant and

XX neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679

XX represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,

XX oligonucleotides and proteins given in the exemplification of the present

XX invention

XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 4; Length 2009;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YMFFVLVIFLGSPFLINILAVVMAY 28
|||
DB 399 YMFFVLVIFLGSPFLINILAVVMAY 426

RESULT 24

AAE20515 ID AAE20515 standard; protein; 2009 AA.

XX AAE20515;

DT 01-JUL-2002 (first entry)

DE Human ion channel protein #6.

XX Human; novel human protein; NHP; voltage-gated sodium channel;

KW gene therapy; bioreactor; mental disorder; biological disorder;

XX medical disorder.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Misc-difference 992 /note= "Encoded by MTG"

FT Misc-difference 1067 /note= "Encoded by RCA"

FT WO200214498-A2.

XX 21-FEB-2002.

XX 15-AUG-2001; 2001WO-US025650.

XX 16-AUG-2000; 2000US-0225989P.

XX (LEXI-) LEXICON GENETICS INC.

XX Turner CA, Mathur B, Mathur D;

XX MPI; 2002-280757/32.

XX N-PSDB; AAD32844.

PT Novel polynucleotides encoding human sodium channel proteins,

PT particularly voltage-gated sodium channel proteins useful for drug

PT screening, diagnosis and in gene therapy of biological disorders.

XX Claim 5; Page 57-62; 83pp; English.

XX The present sequence is novel human protein (NHP), ion channel protein.

XX NHP share structural similarity with mammalian sodium channel proteins

XX particularly voltage-gated sodium channel proteins. NHP oligonucleotides

XX are useful as hybridisation probes for screening libraries and assessing

XX gene expression patterns. Sequences derived from regions adjacent to the

XX intron/exon boundaries of NHP gene can be used to design primers for use

XX in amplification assays to detect mutations within the exons, splice

XX sites, introns that can be used in diagnostics and pharmacogenomics. NHP

XX nucleotide sequences are useful for drug screening effective in the

XX treatment of symptomatic or phenotypic manifestations of perturbing the

XX normal function of NHP in the body, and nucleotide constructs encoding

XX NHP products are useful to genetically engineer host cells to express NHP

XX products in vivo. These genetically engineered cells function as

XX bioreactors in the body delivering a continuous supply of a NHP, a NHP

XX peptide, or a NHP fusion protein to the body. Nucleotide construct

XX encoding NHP products are also useful in gene therapy for modulating NHP

XX expression and to produce genetically engineered host cells to express

XX NHP products in vivo. NHP nucleotide sequences may also be used as part

CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YMIFVLVIFLGSFYLINILAVVAMAY 28
DB 399 YMIFVLVIFLGSFYLINILAVVAMAY 426

RESULT 25

ABG69292 ID ABG69292 standard; protein; 2009 AA.

AC ABG69292;

DT 21-OCT-2002 (first entry)

DE Human sodium channel alpha 1-subunit (SCNA1) variant protein #4.

KW Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;

KW generalised epilepsy with febrile seizures plus; myasthenia;

KW sodium channel dysfunction; malignant hyperthermia; neuropathic pain;

KW inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;

KW schizophrenia; hyperkplexia; anticonvulsant; analgesic; neuroprotective;

KW nootropic; anti-Parkinsonian; neuroleptic.

XX Homo sapiens.

OS

PN W0200250096-A1.

XX 27-JUN-2002.

PD 20-DEC-2001; 2001WO-AU001648.

XX 20-DEC-2000; 2000AU-00002203.

PR (BION-) BIONOMICS LTD.

XX Wallace RH, Mulley JC, Berkovic SF;

PI WPI; 2002-528445/56.

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Query Match 100.0%; Score 28; DB 5; Length 2009;
Best Local Similarity 100.0%; Pred. No. 1.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YMIFVLVIFLGSFYLINILAVVAMAY 28
DB 399 YMIFVLVIFLGSFYLINILAVVAMAY 426

Search completed: January 27, 2005, 17:45:13
Job time : 90.5 secs

Claim 53; Page 147-157; 198pp; English.

The invention relates to a nucleic acid molecule encoding a mutant alpha subunit of a mammalian voltage-gated sodium channel. The DNA and the polypeptide may be used in the diagnosis of epilepsy, in particular generalised epilepsy with febrile seizures plus, and other disorders associated with sodium channel dysfunction. The polypeptide is useful for the screening of candidate pharmaceutical agents, where high throughput screening techniques are employed. The sequences are also useful in the manufacture of a medicament for the treatment of a disorder associated with sodium channel dysfunction such as epilepsy, particularly generalised epilepsy with febrile seizures plus, malignant hyperthermia, myasthenia, episodic ataxia, neuropathic and inflammatory pain, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperkplexia and myotonia. Sequences ABG69289-ABG69293 represent human sodium channel alpha 1-subunit (SCNA1) polypeptides of the invention

Sequence 2009 AA;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:05 : Search time 17 Seconds
(without alignments)
158.475 Million cell updates/sec

Title: US-10-608-584-1
Perfect score: 28
Sequence: 1 YMIFPVLVIFLGSFYLINILNAVAMAY 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	2005	2 A46269	sodium channel alp
2	28	100.0	2005	2 B25019	sodium channel pro
3	28	100.0	2009	2 A25019	sodium channel pro
4	21	75.0	1820	1 CHEE	sodium channel pro
5	21	75.0	1977	2 S54771	sodium channel alp
6	21	75.0	2049	2 T43161	sodium channel pro
7	20	71.4	1835	2 I54323	sodium channel alp
8	20	71.4	1836	2 I64893	sodium channel alp
9	20	71.4	1836	2 J50648	sodium channel alp
10	20	71.4	1836	2 I51964	sodium channel alp
11	20	71.4	1840	1 CHRTM1	sodium channel pro
12	16	57.1	1951	2 S00320	sodium channel pro
13	16	57.1	1983	2 A60054	sodium channel pro
14	13	46.4	1957	2 S68453	sodium channel pro
15	13	39.3	1976	2 I56555	sodium channel pro
16	11	39.3	2016	2 A38195	sodium channel pro
17	11	39.3	2019	2 A33996	sodium channel pro
18	10	35.7	1784	2 T43167	sodium channel pro
19	9	32.1	286	2 S16294	chlorophyll a/b-bi
20	9	32.1	286	2 S2186	chlorophyll a/b-bi
21	9	32.1	1765	2 T42388	sodium channel alp
22	8	28.6	103	2 A53461	voltage-sensitive
23	8	28.6	245	2 T15794	hypothetical prote
24	8	28.6	575	2 D69611	ABC transporter re
25	8	28.6	1034	2 S60051	sodium channel alp
26	8	28.6	1034	2 S60060	sodium channel alp
27	8	28.6	1321	2 A60165	sodium channel pro
28	8	28.6	1689	2 S72467	sodium channel pro
29	8	28.6	1820	2 A33299	sodium channel pro

30	8	28.6	2108	2 S72458	sodium channel pro
31	7	25.0	211	2 F70029	conserved hypothet
32	7	25.0	308	2 J2C253	chitinase (EC 3.2.
33	7	25.0	318	2 S14948	chitinase (EC 3.2.
34	7	25.0	349	2 A72605	probable high-affi
35	7	25.0	361	2 T33402	hypothetical prote
36	7	25.0	365	1 S77076	phospho-N-acetylmu
37	7	25.0	376	2 A36978	MAP kinase mpk-1 (
38	7	25.0	444	2 A36977	MAP kinase sur-1 (
39	7	25.0	724	2 B85045	probable calcium c
40	7	25.0	800	2 T26583	hypothetical prote
41	7	25.0	844	2 B69000	cation-transportin
42	7	25.0	1217	2 C86159	hypothetical prote
43	6	21.4	50	2 D91083	hypothetical prote
44	6	21.4	51	2 I61238	heparin-binding ep
45	6	21.4	59	2 S56139	membrane protein n
46	6	21.4	72	2 AH0039	probable exported
47	6	21.4	82	2 B43702	X'82 protein - Afr
48	6	21.4	84	2 S27162	heparin-binding ep
49	6	21.4	103	1 BVYCGS	chaperonin groES -
50	6	21.4	103	2 A36721	hypothetical prote
51	6	21.4	106	2 D69931	hypothetical prote
52	6	21.4	106	2 T22069	NADH2 dehydrogenas
53	6	21.4	115	2 T17085	V18 protein - Afr
54	6	21.4	118	2 I45348	LIS121-1 protein -
55	6	21.4	121	2 A36821	LIS124-2 protein -
56	6	21.4	124	2 B36821	LIS124-1 protein -
57	6	21.4	124	2 C36821	membrane protein -
58	6	21.4	124	2 C43702	membrane protein Y
59	6	21.4	135	2 T05909	probable auxin-ind
60	6	21.4	141	2 A86417	cytochrome c oxida
61	6	21.4	157	2 D83742	hypothetical prote
62	6	21.4	159	2 B70635	hypothetical prote
63	6	21.4	166	2 D70553	hypothetical prote
64	6	21.4	181	2 B84121	hypothetical prote
65	6	21.4	189	2 T02423	probable low tempe
66	6	21.4	197	2 T07995	ycf4 protein - Chl
67	6	21.4	201	2 G72663	hypothetical prote
68	6	21.4	201	2 G90385	hypothetical prote
69	6	21.4	208	1 A38432	heparin-binding EG
70	6	21.4	208	1 A41914	diphtheria toxin re
71	6	21.4	213	2 A75218	hypothetical prote
72	6	21.4	215	2 I38473	olfactory receptor
73	6	21.4	218	2 G95016	conserved hypothet
74	6	21.4	227	2 B81054	deda protein, prob
75	6	21.4	227	2 B70790	hypothetical prote
76	6	21.4	234	2 A70131	phosphatidylytransf
77	6	21.4	238	2 T33550	hypothetical prote
78	6	21.4	240	2 H97783	hypothetical prote
79	6	21.4	246	2 S15378	H+-transporting tw
80	6	21.4	247	2 T11315	ATP synthase chain
81	6	21.4	249	2 T27019	hypothetical prote
82	6	21.4	252	2 B98204	probable permease
83	6	21.4	252	2 AF3082	hypothetical prote
84	6	21.4	254	1 G69878	conserved hypothet
85	6	21.4	259	2 B83419	conserved hypothet
86	6	21.4	261	2 B81823	Deda-family integr
87	6	21.4	261	2 B90107	putative CCR4-asso
88	6	21.4	266	2 C87367	flagellar biosynth
89	6	21.4	273	2 T37841	probable transloca
90	6	21.4	273	2 A11864	hypothetical prote
91	6	21.4	276	2 A72276	phosphate ABC tran
92	6	21.4	279	2 D89784	hypothetical prote
93	6	21.4	280	2 D84015	maltose/maltodextr
94	6	21.4	282	2 A10948	hypothetical prote
95	6	21.4	283	2 E83902	maltose/maltodextr
96	6	21.4	284	2 AC2551	hypothetical prote
97	6	21.4	284	2 E97054	spontaneous protei
98	6	21.4	288	2 T37395	probable 33.6k pro
99	6	21.4	288	2 A42518	A8r protein - vacc
100	6	21.4	288	2 F72164	A9r protein - vari

ALIGNMENTS

RESULT 1

A46269
sodium channel alpha chain HBA - human
C/Species: Homo sapiens (man)
C/Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
C/Accession: A46269
R/Almed, C.M.; Ware, D.H.; Lee, S.C.; Patten, C.D.; Ferrer-Montiel, A.V.; Schinder, A.F.
Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992
A/Title: Primary structure, chromosomal localization, and functional expression of a voltage-gated sodium channel from human brain
A/Reference number: A46269; MUID:92390418; PMID:1325650
A/Accession: A46269
A/Molecule type: mRNA
A/Residues: 1-2005 <AHM>
A/Cross-references: GB:M94055
A/Experimental source: brain
A/Note: sequence extracted from NCBI backbone (NCBIP:113082)
C/Genetics:
A/Map position: 2q23-q24.3
C/Superfamily: sodium channel protein
C/Keywords: duplication

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 2005;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 YMIFFVLVIFLGSFYILNIIILAVVAMAY 28
DB 401 YMIFFVLVIFLGSFYILNIIILAVVAMAY 428

RESULT 2

B25019
sodium channel protein II - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: B25019; S24804
R/Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H.
Nature 320, 188-192, 1986
A/Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A/Reference number: A93377; MUID:86146901; PMID:3754035
A/Accession: B25019
A/Molecule type: mRNA
A/Residues: 1-2005 <NOD>
A/Cross-references: UNIPROT:Q63509
A/Experimental source: brain
R:Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
Submitted to the EMBL Data Library, August 1991
A/Description: Developmentally regulated RNA splicing of rat brain sodium channel mRNAs.
A/Reference number: S24803
A/Accession: S24804
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 183-188, 'D', 190-305 <SAR>
A/Cross-references: EMBL:X61149; NID:957074; PIDN:CAA43458.1; PID:957076
C/Superfamily: sodium channel protein
C/Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

QY

Best Local Similarity 100.0%; Score 28; DB 2; Length 2005;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 YMIFFVLVIFLGSFYILNIIILAVVAMAY 28
DB 401 YMIFFVLVIFLGSFYILNIIILAVVAMAY 428

Query Match 100.0%; Score 28; DB 2; Length 2005;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

A25019
sodium channel protein I - rat
N/Alternate names: sodium channel protein A

C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C/Accession: A25019; S40783; I84764
R/Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H.
Nature 320, 188-192, 1986
A/Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A/Reference number: A93377; MUID:86146901; PMID:3754035
A/Accession: A25019
A/Molecule type: mRNA
A/Residues: 1-2009 <NOD>
A/Cross-references: UNIPROT:P04774; GB:X03638; NID:957216; PIDN:CAA27286.1; PID:957217
A/Experimental source: brain
R:Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.
Nucleic Acids Res. 19, 5673-5679, 1991
A/Title: Developmentally regulated alternative RNA splicing of rat brain sodium channel
A/Reference number: S40783; MUID:92051314; PMID:1658739
A/Accession: S40783
A/Molecule type: DNA
A/Residues: 177-253 <SAR>
R/Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A/Title: Structure and function of sodium channel.
A/Reference number: I50536; MUID:87311395; PMID:2442385
A/Accession: I84764
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2009 <RES>
A/Cross-references: GB:M22253; NID:91041088; PIDN:AAA79965.1; PID:91041089
C/Superfamily: sodium channel protein
C/Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

QY

Best Local Similarity 100.0%; Score 28; DB 2; Length 2009;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 YMIFFVLVIFLGSFYILNIIILAVVAMAY 28
DB 399 YMIFFVLVIFLGSFYILNIIILAVVAMAY 426

RESULT 4

CHER
sodium channel protein - electric eel
C/Species: Electrophorus electricus (Electric eel)
C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C/Accession: A03178; I50536
R/Noda, M.; Shimizu, S.; Tanabe, T.; Takai, T.; Kayano, T.; Ikeda, T.; Takahashi, H.; Numa, S.
Nature 312, 121-127, 1984
A/Title: Primary structure of Electrophorus electricus sodium channel deduced from cDNA
A/Reference number: A03178; MUID:85061498; PMID:6209577
A/Accession: A03178
A/Molecule type: mRNA
A/Residues: 1-1820 <NOD>
A/Cross-references: UNIPROT:P02719; GB:X01119; NID:962776; PIDN:CAA25587.1; PID:962777
R/Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A/Title: Structure and function of sodium channel.
A/Reference number: I50536; MUID:87311395; PMID:2442385
A/Accession: I50536
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1820 <NOD>
A/Cross-references: GB:M22252; NID:91041048; PIDN:AAA79960.1; PID:91041049
C/Comment: This membrane glycoprotein mediates the voltage-dependent sodium-ion permeability of the membrane, the protein forms a sodium-selective channel through which sodium ions pass. This sequence contains four highly homologous internal repeats (excluding repeats 1 and 2) which have a net positive charge (S4), and one is neutral (S2).
C/Comment: The four repeating units are thought to be oriented pseudosymmetrically across the membrane.
C/Comment: Available data suggest that activation and inactivation gates are located near the extracellular side, in conjunction with the positively charged residues of S4, act as a voltage sensor.

C:Superfamily: sodium channel protein
C:Keywords: duplication; glycoprotein; ion transport; membrane protein; sodium channel;
F:111-419,555-587,989-1281,1311-1341/Region: duplication internal repeats I, II, III and
F:111-141,555-585,989-1019,1311-1341/Region: S1 of repeats I through IV
F:150-171,597-620,1033-1057,1153-1376/Region: S2 of repeats I through IV
F:177-197,628-643,1062-1079,1181-1398/Region: S3 of repeats I through IV
F:204-224,651-671,1092-1112,1417-1437/Region: S4 of repeats I through IV
F:244-264,691-711,1132-1152,1454-1474/Region: S5 of repeats I through IV
F:379-402,767-790,1236-1264,1544-1567/Region: S6 of repeats I through IV
F:205,278,288,317,591,690,797,1160,1174,1806/Binding site: carbohydrate (Asn) (covalent)

Query Match 75.0%; Score 21; DB 1; Length 1820;
Best Local Similarity 100.0%; Pred. No. 1.5e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VFLLGSFYILNLIILAVVAMAY 28
|||||
DB 385 VFLLGSFYILNLIILAVVAMAY 405

RESULT 5
S54771
sodium channel alpha subunit - human
C:Species: Homo sapiens (man)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S54771
R:Kluebauer, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.
EMBO J. 14, 1084-1090, 1995
A:Title: Structure and functional expression of a new member of the tetrodotoxin-sensitive
A:Reference number: S54771; PMID:95237189; PMID:7720699
A:Accession: S54771
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1977 <KUL>
A:Cross-references: UNIPROT:Q15858, EMBL:X62835, NID:9756109, PIDN:CAA58042.1; PID:97561
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query Match 75.0%; Score 21; DB 2; Length 1977;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VFLLGSFYILNLIILAVVAMAY 28
|||||
DB 385 VFLLGSFYILNLIILAVVAMAY 405

RESULT 6
T43161
sodium channel protein Tuna1 - sea squirt (Halocynthia roretzi)
C:Species: Halocynthia roretzi
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43161
R:Okamura, Y.; Ono, F.; Okagaki, R.; Chong, J.; Mandel, G.
Neuron 13, 937-948, 1994
A:Title: Neutral expression of a sodium channel gene requires cell-specific interactions.
A:Reference number: 22320; PMID:95033215; PMID:794638
A:Accession: T43161
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2049 <OKA>
A:Cross-references: UNIPROT:Q25150; EMBL:DJ7311; PIDN:BA04133.1
C:Superfamily: sodium channel protein
C:Keywords: sodium channel; transmembrane protein

Query Match 75.0%; Score 21; DB 2; Length 2049;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VFLLGSFYILNLIILAVVAMAY 28
|||||
DB 449 VFLLGSFYILNLIILAVVAMAY 469

RESULT 7
154323
sodium channel alpha subunit - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: 154323
R:McClatchey, A.L.; Lin, C.S.; Wang, J.; Hoffman, E.P.; Rojas, C.; Gueelle, J.F.
Hum. Mol. Genet. 1, 521-527, 1992
A:Title: The genomic structure of the human skeletal muscle sodium channel gene.
A:Reference number: 154323; PMID:9335844; PMID:1339144
A:Accession: 154323
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1835 <RES>
A:Cross-references: GB:J01983, NID:9337992, PIDN:AAA75557.1, PID:9308809
C:Genetics:
A:Gene: GDB:SCN4A
A:Cross-references: GDB:125181, OMIM:170500
A:Map position: 17q23.1-17q25.3
A:Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3;
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query Match 71.4%; Score 20; DB 2; Length 1835;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFLLGSFYILNLIILAVVAMAY 28
|||||
DB 431 IFLLGSFYILNLIILAVVAMAY 450

RESULT 8
164893
sodium channel alpha subunit - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: 164893
R:George, A.L.
Ann. Neurol. 31, 131-137, 1992
A:Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium
A:Reference number: 151964; PMID:92246457; PMID:115496
A:Accession: 164893
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1836 <RES>
A:Cross-references: UNIPROT:P35499, GB:W81758, NID:9338212, PIDN:AAA60554.1, PID:933821.
C:Genetics:
A:Gene: SKM1
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query Match 71.4%; Score 20; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFLLGSFYILNLIILAVVAMAY 28
|||||
DB 431 IFLLGSFYILNLIILAVVAMAY 450

RESULT 9
J50648
sodium channel alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: J50648; J42099
R:Yang, J.; Rojas, C.V.; Zhou, J.; Schwartz, L.S.; Nicholas, H.; Hofmann, E.P.
Biochem. Biophys. Res. Commun. 182, 794-801, 1992
A:Title: Sequence and genomic structure of the human adult skeletal muscle sodium channe
A:Reference number: J50648; PMID:92134303; PMID:1310396
A:Accession: J50648

A:Residues: 1-1836 <RES>
A:Cross-references: UNIPROT:P35499; GB:J04236; NID:g232485; PIDN:AAB59624.1; PID:g292487
A:Genetics:
A:Gene: GDB:SCN4A
A:Cross-references: GDB:125181; OMIM:170500
A:Map position: 17q23.1-17q25.3
A:Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3;
C:Superfamily: sodium channel protein
C:Keywords: duplication; skeletal muscle

Query Match 71.4%; Score 20; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 431 IFLGSPYLNLILAVVAMAY 450

QY 9 IFLGSPYLNLILAVVAMAY 28
|||||
425 IFLGSPYLNLILAVVAMAY 444

RESULT 11

CHR1M1
sodium channel protein mul alpha chain, skeletal muscle - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
A:Accession: JN0007
R:Trimmer, J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.; Kal1
N:urion 3,33-44, 1989
A:Title: Primary structure and functional expression of a mammalian skeletal muscle sodi
A:Reference numbers: JN0007; MUID:90148778; PMID:2559760
A:Accession: JN0007
A:Molecule type: mRNA
A:Residues: 1-1840 <TRI>
A:Cross-references: UNIPROT:P15390; GB:M26643; NID:g205651; PIDN:AAA41682.1; PID:g205652
C:Comment: Action potentials propagated by skeletal muscle sodium channels are responsib
C:Comment: This heavily glycosylated protein contains four homologous domains, each of w
C:Superfamily: sodium channel protein
C:Keywords: duplication; glycoprotein; ion transport; neuromuscular junction; phosphopro
F:120-458,561-813,1013-1305,1335-1611/Region: duplication (by cAMP-dependent kinase) #
F:56,251,1321,1504/Binding site: phosphate (Ser)
F:214,288,291,297,303,309,315,327,356,502,696,954,1184,1198,1563,1702/Binding site: carb

Query Match 71.4%; Score 20; DB 1; Length 1840;
Best Local Similarity 100.0%; Pred. No. 1.4e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFLGSPYLNLILAVVAMAY 28
|||||
425 IFLGSPYLNLILAVVAMAY 444

RESULT 12

S00320
sodium channel protein III - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
A:Accession: S00320
R:Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S.
FEBS Lett. 228, 187-194, 1988
A:Title: Primary structure of rat brain sodium channel III deduced from the cDNA sequenc
A:Reference numbers: S00320; MUID:86137594; PMID:2449363
A:Accession: S00320
A:Molecule type: mRNA
A:Residues: 1-1951 <RAY>
A:Cross-references: UNIPROT:P08104; EMBL:Y00766; NID:g57210; PIDN:CAA68735.1; PID:g57211
C:Superfamily: sodium channel protein
C:Keywords: duplication; transmembrane protein

Query Match 57.1%; Score 16; DB 2; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16

QY 1 YMFVFLVFLGSPYL 16
 |||||
 Db 400 YMFVFLVFLGSPYL 415

RESULT 13

A60054

sodium channel protein IIB, long form - rat
 C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004

C:Accession: A60054; B44824

C:Joho, R.H.; Moorman, J.R.; Vandongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster, Brain Res. Mol. Brain Res. 7, 105-113, 1990

A>Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in X

A:Reference number: A60054; MUID:90251117; PMID:2160038

A:Accession: A60054

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-1983 <JOH>

A:Cross-references: UNIPROT:064243

R:Schaller, K.L.; Krzemien, D.M.; McKenna, N.M.; Caldwell, J.H.

J. Neurosci. 12, 1370-1381, 1992

A>Title: Alternatively spliced sodium channel transcripts in brain and muscle.

A:Reference number: A44824; MUID:92211397; PMID:1313493

A:Accession: B44824

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 611-662 <SCH>

A:Cross-references: GB:S97388; NID:G248225; PIDN:AA821984.1; PID:G248226

A:Experimental source: skeletal muscle

A>Note: sequence inconsistent with the nucleotide translation

C:Superfamily: sodium channel protein

C:Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane proc

Query Match 57.1%; Score 16; DB 2; Length 1983;

Best Local Similarity 100.0%; Pred. No. 1.2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMFVFLVFLGSPYL 16
 |||||
 Db 400 YMFVFLVFLGSPYL 415

RESULT 14

sodium channel protein SNS - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: S68453

R:Akopian, A.N.; Sivijott, L.; Wood, J.N.

Nature 379, 257-262, 1996

A>Title: A tetrodotoxin-resistant voltage-gated sodium channel expressed by sensory neur

A:Reference number: S68453; MUID:96138382; PMID:8538791

A:Accession: S68453

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1957 <AKO>

A:Cross-references: UNIPROT:063554; GB:X92184; NID:G1209466; PIDN:CAA63095.1; PID:G12094

A:Experimental source: dorsal root ganglia

C:Superfamily: sodium channel protein

C:Keywords: sodium channel; transmembrane protein; voltage-gated ion channel

F:113-148/Domain: transmembrane #status predicted <TM1>

F:158-174/Domain: transmembrane #status predicted <TM2>

F:123-241/Domain: transmembrane #status predicted <TM3>

F:249-265/Domain: transmembrane #status predicted <TM4>

F:376-392/Domain: transmembrane #status predicted <TM5>

F:666-688/Domain: transmembrane #status predicted <TM6>

F:702-718/Domain: transmembrane #status predicted <TM7>

F:731-747/Domain: transmembrane #status predicted <TM8>

F:788-804/Domain: transmembrane #status predicted <TM9>

F:865-881/Domain: transmembrane #status predicted <TM10>

F:1194-1210/Domain: transmembrane #status predicted <TM12>
 F:1221-1237/Domain: transmembrane #status predicted <TM13>
 F:1286-1302/Domain: transmembrane #status predicted <TM14>
 F:1400-1416/Domain: transmembrane #status predicted <TM15>
 F:1482-1498/Domain: transmembrane #status predicted <TM16>
 F:1516-1532/Domain: transmembrane #status predicted <TM17>
 F:1546-1562/Domain: transmembrane #status predicted <TM18>
 F:1606-1622/Domain: transmembrane #status predicted <TM19>
 F:1708-1724/Domain: transmembrane #status predicted <TM20>

Query Match 46.4%; Score 13; DB 2; Length 1957;

Best Local Similarity 100.0%; Pred. No. 9.6e-05;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FFLVFLGSPYL 16
 |||||
 Db 375 FFLVFLGSPYL 387

RESULT 15

sodium channel protein 6 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56555

R:Schaller, K.L.; Krzemien, D.M.; Yarowsky, P.J.; Krueger, B.K.; Caldwell, J.H.

J. Neurosci. 15, 3231-3242, 1995

A>Title: A novel, abundant sodium channel expressed in neurons and glia.

A:Reference number: I56555; MUID:95271284; PMID:7751906

A:Accession: I56555

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1976 <RES>

A:Cross-references: UNIPROT:063541; GB:J39018; NID:9829033; PIDN:AA642059.1; PID:982903

C:Genetics:

A:Gene: SCP6

C:Superfamily: sodium channel protein

C:Keywords: duplication

Query Match 39.3%; Score 11; DB 2; Length 1976;

Best Local Similarity 100.0%; Pred. No. 0.0086;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NLLAVVAMAY 28
 |||||
 Db 405 NLLAVVAMAY 415

RESULT 16

sodium channel protein hH, cardiac - human

N:Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-I Na

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A38195

R:Cellene, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Bacht, R.L.; Kai.

Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992

A>Title: Primary structure and functional expression of the human cardiac tetrodotoxin-

A:Reference number: A38195; MUID:92115699; PMID:1309946

A:Accession: A38195

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-2016 <GEL>

A:Cross-references: UNIPROT:Q14524; GB:M77235; NID:G184038; PIDN:AAA58644.1; PID:G18403

A:Experimental source: heart

C:Superfamily: sodium channel protein

C:Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium char

Query Match 39.3%; Score 11; DB 2; Length 2016;

Best Local Similarity 100.0%; Pred. No. 0.0087;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NLLAVVAMAY 28

Db 406 NLILAVVAMAY 416

RESULT 17

sodium channel protein I, cardiac - rat
A:Accession: A33996

N:Alternate names: sodium channel protein (SKM2) alpha chain
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004

C:Accession: A33996; U00412
R:Rogart, R.B.; Cribbs, L.L.; Muglia, L.K.; Kephart, D.D.; Kaiser, M.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 8170-8174, 1989

A:Title: Molecular cloning of a putative tetrodotoxin-resistant rat heart Na(+) channel
A:Reference number: A33996; PMID:90046760; PMID:25543302
A:Accession: A33996

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2019 <ROG>

A:Cross-references: UNIPROT:P15389; GB:M27902; NID:9206857; PIDN:AAA42114.1; PID:9206858
R:Kallen, R.G.; Sheng, Z.H.; Yang, J.; Chen, L.; Rogart, R.B.; Barchi, R.L.
Neuron 4, 233-242, 1990

A:Title: Primary structure and expression of a sodium channel characteristic of denervat
A:Reference number: U00412; PMID:9016613; PMID:2155010
A:Accession: U00412

A:Molecule type: mRNA
A:Residues: 1-479, 481-1712, 'T', 1714-1963, 'R', 1965-2019 <KAL>
A:Experimental source: muscle
C:Superfamily: sodium channel protein

C:Keywords: cardiac muscle; duplication; heart; sodium channel; transmembrane protein

Query Match 39.3%; Score 11; DB 2; Length 2019;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 407 NLILAVVAMAY 417

RESULT 18

sodium channel protein - California market squid
C:Species: Loligo opalescens (California market squid)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C:Accession: T43167
R:Rosenthal, J.J.; Gilly, W.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 10026-10030, 1993

A:Title: Amino acid sequence of a putative sodium channel expressed in the giant axon of
A:Reference number: Z22324; PMID:94052096; PMID:8234251
A:Accession: T43167

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1784 <ROS>

A:Cross-references: UNIPROT:Q25377; EMBL:L19979; NID:9349118; PID:9349119; PIDN:AAA16202
A:Experimental source: stellate ganglia
C:Superfamily: sodium channel protein

C:Keywords: ion transport; membrane protein; sodium channel; voltage-gated ion channel

Query Match 35.7%; Score 10; DB 2; Length 1784;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 383 LVIFLGSPYL 392

RESULT 19

chlorophyll a/b-binding protein type I precursor - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C:Accession: S16294
R:Pickersky, E.; Subramaniam, R.; White, M.J.; Reid, J.; Aebbersold, R.; Green, B.R.
Mol. Gen. Genet. 227, 277-284, 1991

A:Title: Chlorophyll a/b binding (CAB) polypeptides of CP29, the internal chlorophyll a
or a second CP29 polypeptide.
A:Reference number: S16294; PMID:91287707; PMID:2062308

A:Accession: S16294
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <GRE>

A:Cross-references: UNIPROT:Q00321
C:Superfamily: chlorophyll a/b-binding protein
C:Keywords: chloroplast; thylakoid

Query Match 32.1%; Score 9; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 175 INILAVVA 183

RESULT 20

chlorophyll a/b-binding protein CP29 precursor - barley
C:Species: Hordeum vulgare (barley)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S21386
R:Sorensen, A.B.; Jensen, B.F.; Gausing, K.
submitted to the EMBL Data Library, October 1991

A:Description: Barley (Hordeum vulgare) gene for CP29, a core chlorophyll a/b binding pr
A:Reference number: S21386
A:Accession: S21386

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <SOR>

A:Cross-references: UNIPROT:Q40039; EMBL:X63052; NID:918957; PIDN:CAA44777.1; PID:918958
C:Genetics:
A:Introns: 70/1; 98/2; 115/2; 155/3; 200/3
C:Superfamily: chlorophyll a/b-binding protein

C:Keywords: chloroplast; thylakoid

Query Match 32.1%; Score 9; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 175 INILAVVA 183

RESULT 21

sodium channel alpha chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T42388
R:DiB-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998

A:Title: NAN, a novel voltage-gated Na channel, is expressed preferentially in periph
A:Reference number: Z22149; PMID:98338024; PMID:9671787
A:Accession: T42388

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1765 <DIR>

A:Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:93372614; PID:93372615; PIDN:AA4
A:Experimental source: strain Sprague-Dawley; dorsal root ganglia
A>Note: preferentially expressed in sensory neurons within dorsal root ganglia and trig
C:Superfamily: sodium channel protein

Query Match 32.1%; Score 9; DB 2; Length 1765;
Best Local Similarity 100.0%; Pred. No. 0.69;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VFILGSFYL 16
|||||||
Db 378 VFILGSFYL 386

RESULT 22
A53461
Voltage-sensitive sodium channel - house fly (fragment)
C:Species: Musca domestica (house fly)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A53461

R:Knippl, D.C.; Doyle, K.E.; Marsella-Herrick, P.A.; Soderlund, D.M.
Proc. Natl. Acad. Sci. U.S.A. 91, 2483-2487, 1994
A:Title: Tight genetic linkage between the kdr insecticide resistance trait and a voltage
A:Reference number: A53461; MUID:94195766; PMID:8146143
A:Contents: NAIDM, insecticide-susceptible
A:Accession: A53461

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-103 <KNT>
A:Cross-references: UNIPROT:Q25439, UNIPROT:Q25440, UNIPROT:Q94615
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIN:146081, NCBIP:146080)
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query Match 28.6%; Score 8; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFILGSFYL 16
|||||||
Db 65 IFILGSFYL 72

RESULT 23
T15794

hypothetical protein C42D8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T15794
R:Hallsworth, K.
submitted to the EMBL Data Library, April 1996
A:Description: The sequence of C. elegans cosmid C42D8.
A:Reference number: Z18405
A:Accession: T15794

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-245 <HAU>
A:Cross-references: UNIPROT:Q18582, EMBL:U56966, NID:G1293844, PID:G1293849, PIRN:AAA987
A:Experimental source: strain Bristol N2; clone C42D8
C:Genetics:
A:Gene: CESP:C42D8.1
A:Map position: X
A:Introns: 16/2; 62/3; 90/3; 123/3; 159/3; 208/3

Query Match 28.6%; Score 8; DB 2; Length 245;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FVLVIFLG 12
|||||||
Db 125 FVLVIFLG 132

RESULT 24
D69611
ABC transporter required for expression of cytochrome bd (ATP-) cydD - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C:Accession: D69611

R:Kunzl, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertei
C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chk
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallazzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M.F
Koester, P.; Konigstein, G.; Krog, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portereit
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scrofano, F.; Sekiguchi, J.; Sekowska, A.; Sero
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, I
A:Authors: Yoshikawa, H.F.; Zumestein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A65580; MUID:98044033; PMID:9384377

A:Accession: D69611
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-575 <KUN>
A:Cross-references: UNIPROT:P94367; GB:299123; GB:AL009126; NID:G2636240; PIRN:CA15899.
A:Experimental source: strain 168
C:Genetics:

A:Gene: cydD
C:Superfamily: ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; P-loop
F:353-546/Domain: ATP-binding cassette homology <ABC>
F:370-377/Region: nucleotide-binding motif A (P-loop)

Query Match 28.6%; Score 8; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVLVIFLG 12
|||||||
Db 18 FVLVIFLG 25

RESULT 25
S60051

sodium channel alpha chain, exon c-containing splice form - fruit fly (Drosophila virilis)
C:Species: Drosophila virilis
C:Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004
C:Accession: S60051
R:Thackeray, J.R.; Ganetzky, B.
Genetics 141, 203-214, 1995
A:Title: Conserved alternative splicing patterns and splicing signals in the Drosophila
A:Reference number: S60051; MUID:96042905; PMID:8536988
A:Accession: S60051

A:Status: nucleic acid sequence not shown
A:Molecule type: nucleic acid
A:Residues: 1-1034 <THA>
A:Cross-references: UNIPROT:Q24714; EMBL:U26343
C:Genetics:

A:Gene: FlyBase:FlyBase:FBgn0015214
A:Cross-references: FlyBase:FBgn0015214
C:Superfamily: sodium channel protein
C:Keywords: alternative splicing; duplication; transmembrane protein
F:306-329/Region: alternatively spliced segment 1 (exon 4) #status experimental
F:330-350/Region: alternatively spliced exon a #status experimental
F:338-545/Region: alternatively spliced segment b (exon 9) #status experimental
F:874-886/Region: alternatively spliced segment e (exon 12) #status experimental
F:887-896/Region: alternatively spliced segment f (exon 13) #status experimental
F:958-982/Region: alternatively spliced segment h (exon 14) #status experimental

Query Match 28.6%; Score 8; DB 2; Length 1034;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFILGSFYL 16
|||||||
Db 188 IFILGSFYL 195

Fri Jan 28 09:32:02 2005

us-10-608-584-1.01i.rpr

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Search completed: January 27, 2005, 17:52:42
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 27, 2005, 17:35:20 ; Search time 92.5 Seconds
(without alignments)
174.167 Million cell updates/sec

Title: US-10-608-584-1
Perfect score: 28
Sequence: 1 YWIFVLVFLGSPYLINLILAVMAY 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	506	2 Q86X25	Q86X25 homo sapien
2	28	100.0	510	2 Q86XY2	Q86XY2 homo sapien
3	28	100.0	1981	2 Q81UJ6	Q81UJ6 homo sapien
4	28	100.0	2005	1 C1N2_HUMAN	Q99250 homo sapien
5	28	100.0	2005	1 C1N2_RAT	P04775 ratu
6	28	100.0	2009	1 C1N1_HUMAN	P35498 homo sapien
7	28	100.0	2009	1 C1N1_RAT	P04774 ratu
8	21	75.0	213	2 Q42419	Q42419 gallu
9	21	75.0	225	2 Q42420	Q42420 gallu
10	21	75.0	247	2 Q91BD6	Q91BD6 takifu
11	21	75.0	1820	1 C1N4_ELEBL	P02719 electrophor
12	21	75.0	1880	2 Q91BF1	Q91BF1 takifu
13	21	75.0	1977	2 Q15858	Q15858 homo sapien
14	21	75.0	1984	2 Q28644	Q28644 oryctolagus
15	21	75.0	1984	2 Q08562	Q08562 ratu
16	21	75.0	2049	2 Q25150	Q25150 halocynthia
17	20	71.4	1836	1 C1N4_HUMAN	P35499 homo sapien
18	20	71.4	1840	1 C1N4_RAT	P15390 ratu
19	20	71.4	1840	1 Q70611	Q70611 ratu
20	20	71.4	1841	2 Q98R60	Q98R60 mus musculu
21	16	57.1	530	2 Q90518	Q90518 fugu rubrip
22	16	57.1	711	2 Q803T8	Q803T8 brachydanto
23	16	57.1	1834	2 Q28371	Q28371 equu
24	16	57.1	1951	1 C1N3_RAT	P08104 ratu
25	16	57.1	1951	2 Q9C007	Q9C007 homo sapien
26	16	57.1	1956	2 Q9Y5Y9	Q9Y5Y9 homo sapien
27	16	57.1	2000	1 C1N3_HUMAN	Q9N746 homo sapien
28	16	57.1	2007	2 Q9YGN7	Q9YGN7 cynops pyrr
29	13	46.4	1956	2 Q62968	Q62968 ratu
30	13	46.4	1957	2 Q6Q1Y3	Q6Q1Y3 mus musculu
31	13	46.4	1957	2 Q63554	Q63554 ratu

32	13	46.4	1957	2 AAS45602	AAS45602 mus muscu
33	13	46.4	1958	2 P70276	P70276 mus musculu
34	13	46.4	1962	2 Q46669	Q46669 canis fami
35	12	42.9	1444	2 Q9UDM0	Q9UDM0 homo sapien
36	12	42.9	1791	2 Q8NDX3	Q8NDX3 homo sapien
37	12	42.9	1791	2 Q9UHE0	Q9UHE0 homo sapien
38	12	42.9	1791	2 Q9U133	Q9U133 homo sapien
39	11	39.3	1136	2 Q804F4	Q804F4 sternopygus
40	11	39.3	1717	2 Q90519	Q90519 fugu rubrip
41	11	39.3	1949	2 Q9DRE3	Q9DRE3 brachydanto
42	11	39.3	1962	2 Q75RX9	Q75RX9 homo sapien
43	11	39.3	1962	2 BAD12085	BAD12085 homo sapi
44	11	39.3	1966	2 Q925G6	Q925G6 ratu
45	11	39.3	1976	2 Q63541	Q63541 ratu
46	11	39.3	1978	1 C1N8_MOUSE	Q9WU33 mus musculu
47	11	39.3	1978	1 Q884Z0	Q884Z0 ratu
48	11	39.3	1980	1 C1N8_HUMAN	Q9UG40 homo sapien
49	11	39.3	1988	2 Q884Z1	Q884Z1 ratu
50	11	39.3	2013	2 Q865W3	Q865W3 canis fami
51	11	39.3	2015	2 Q86UR3	Q86UR3 homo sapien
52	11	39.3	2015	2 Q81XC9	Q81XC9 homo sapien
53	11	39.3	2015	2 Q96369	Q96369 homo sapien
54	11	39.3	2016	1 C1N5_HUMAN	Q14524 homo sapien
55	11	39.3	2016	2 Q75RY0	Q75RY0 homo sapien
56	11	39.3	2016	2 BAD12084	BAD12084 homo sapi
57	11	39.3	2019	1 C1N5_RAT	P15389 ratu
58	11	39.3	2019	2 Q9JUV9	Q9JUV9 mus musculu
59	11	39.3	2022	2 Q8WMP8	Q8WMP8 bos taurus
60	10	35.7	207	2 Q42421	Q42421 gallu
61	10	35.7	211	2 Q42418	Q42418 gallu
62	10	35.7	1784	2 Q25377	Q25377 loigo opal
63	9	32.1	286	2 Q00321	Q00321 lycopersico
64	9	32.1	286	2 Q40039	Q40039 hordeum vul
65	9	32.1	1765	2 Q88457	Q88457 ratu
66	9	32.1	1765	2 Q9JMD4	Q9JMD4 mus musculu
67	9	32.1	1765	2 Q9R053	Q9R053 mus musculu
68	8	28.6	60	2 Q8N0R3	Q8N0R3 pluteia xy
69	8	28.6	65	2 Q868A9	Q868A9 drosophila
70	8	28.6	80	2 Q7KQ27	Q7KQ27 heliothis v
71	8	28.6	269	2 Q18582	Q18582 caenorhabdi
72	8	28.6	305	2 Q7JPG9	Q7JPG9 drosophila
73	8	28.6	329	2 Q24719	Q24719 drosophila
74	8	28.6	362	2 Q7JN89	Q7JN89 drosophila
75	8	28.6	501	2 Q6DLT8	Q6DLT8 aedes albop
76	8	28.6	509	2 Q6DLT7	Q6DLT7 aedes albop
77	8	28.6	525	2 Q6DLT9	Q6DLT9 aedes albop
78	8	28.6	530	2 Q6DLU0	Q6DLU0 aedes aegypt
79	8	28.6	575	1 CYDD_BACSU	Q94367 bacillus su
80	8	28.6	1087	2 Q9XYM6	Q9XYM6 lepicinctars
81	8	28.6	1538	2 Q7PE76	Q7PE76 drosophila
82	8	28.6	1618	2 Q8WMC7	Q8WMC7 anopheles g
83	8	28.6	1689	2 Q93135	Q93135 blattella g
84	8	28.6	1695	2 Q94584	Q94584 heliothis v
85	8	28.6	2031	2 Q01306	Q01306 blattella g
86	8	28.6	2031	2 Q61307	Q61307 blattella g
87	8	28.6	2051	2 Q86D17	Q86D17 pediculus h
88	8	28.6	2051	2 Q86D18	Q86D18 pediculus h
89	8	28.6	2051	2 Q86D19	Q86D19 pediculus h
90	8	28.6	2058	2 Q6DLT4	Q6DLT4 aedes albop
91	8	28.6	2064	2 Q6DLT3	Q6DLT3 aedes aegypt
92	8	28.6	2086	2 Q86M38	Q86M38 pediculus h
93	8	28.6	2104	2 Q25440	Q25440 musca domes
94	8	28.6	2105	2 Q25439	Q25439 musca domes
95	8	28.6	2108	2 Q94615	Q94615 musca domes
96	8	28.6	2131	1 C1N4_DROME	P35500 drosophila
97	8	28.6	2215	2 Q86D77	Q86D77 varroa destruct
98	8	28.6	2223	2 Q7Q1V0	Q7Q1V0 anopheles g
99	8	28.6	2304	2 Q9BMQ4	Q9BMQ4 blattella g
100	8	28.6	2327	2 Q9W0Y8	Q9W0Y8 drosophila

ALIGNMENTS

RESULT 1

Q86X25 PRELIMINARY; PRT; 506 AA.
 AC Q86X25
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to sodium channel, voltage-gated, type II, alpha 2 polypeptide (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR HSSP; P08104; 1Q99.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M+channel_nlg.
 DR Pfam; PF00520; Ion_trans_1.
 DR Ion transport; Ionic channel; Transmembrane; Transport.
 KW NON_TER
 FT SEQUENCE 506 AA; 57147 MW; 39C32369D2A6D9 CRC64;

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 506;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMIFFVLVIFLGSFYILNLIIVAVMAY 28
 Db 401 YMIFFVLVIFLGSFYILNLIIVAVMAY 428

RESULT 2

Q86X25 PRELIMINARY; PRT; 510 AA.
 AC Q86X25
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to sodium channel, voltage-gated, type II, alpha 2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR HSSP; P08104; 1Q99.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M+channel_nlg.
 DR Pfam; PF00520; Ion_trans_1.
 DR Ion transport; Ionic channel; Transmembrane; Transport.
 KW NON_TER
 FT SEQUENCE 510 AA; 57660 MW; CFB153E259C32369 CRC64;

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 510;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2.6e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMIFFVLVIFLGSFYILNLIIVAVMAY 28
 Db 401 YMIFFVLVIFLGSFYILNLIIVAVMAY 428

RESULT 3

Q8IUU6 PRELIMINARY; PRT; 1981 AA.
 AC Q8IUU6
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Voltage-gated sodium channel alpha 1 subunit.
 GN Name=SCN1A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Normal brain;
 RA Ouchida M.; Ohmori T.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; AB098335; BAC45228.1; -.
 DR HSSP; P04775; 1BYX.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0005248; P:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_Typl.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR008051; Na_channel.
 DR InterPro; IPR00526; Na_trans_assoc.
 DR InterPro; IPR000100; Ribonuclease_P.
 DR Pfam; PF00520; Ion_trans; 4.
 DR Pfam; PF00612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR PRINTS; PR01664; NACHANNEL1.
 DR SMART; SM00015; IQ_1.
 DR PROSITE; PS00648; RIBONUCLEASE_P; UNKNOWN_1.
 DR Ion transport; Ionic channel; Sodium channel; Transmembrane; Transport; Voltage-gated channel.
 KW TRANSPORT
 FT SEQUENCE 1981 AA; 226201 MW; BID6946D6491B7AD CRC64;

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 1981;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YMIFFVLVIFLGSFYILNLIIVAVMAY 28
 Db 399 YMIFFVLVIFLGSFYILNLIIVAVMAY 426

RESULT 4

CIN2_HUMAN STANDARD; PRT; 2005 AA.
 ID CIN2_HUMAN
 AC Q99250; Q14472; Q9BZC9; Q9BZD0;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel protein type II alpha subunit (Voltage-gated sodium

DE channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
 DR subunit) (HSC II).
 GN Name=SCN2A; Synonyms=SCN2A2, NAC2;
 OS Homo sapiens (Human)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=92390418; PubMed=1325650;
 RA Ahmed C.M., Ware D.H., Lee S.C., Patten C.D., Ferrer-Montiel A.V.,
 RA Schinder A.F., McPherson J.D., Wagner-McPherson C.B., Wasmuth J.O.,
 RA Evans G.A., Montal M.;
 RT "Primary structure, chromosomal localization, and functional
 RT expression of a voltage-gated sodium channel from human brain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:8220-8224(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
 RA Kasai N., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
 RA Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
 RT "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
 RT at the DFNA16 locus.";
 RL Gene 264:113-122(2001).
 RN [3]
 RP SEQUENCE OF 1-89 FROM N.A.
 RA Lu C.-M., Eichelberger J.S., Beckman M.L., Schade S.D., Brown G.B.;
 RT "Isolation of the 5'-flanking region for human brain sodium channel
 RT subtype II alpha-subunit (SCN2A).";
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1702-2005 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92275082; PubMed=1317301;
 RA Lu C.-M., Han J., Rado T.A., Brown G.B.;
 RT "Differential expression of two sodium channel subtypes in human
 RT brain.";
 RL FEBS Lett. 303:53-58(1992).
 RN [5]
 RP SEQUENCE OF 1702-1772 FROM N.A.
 RX MEDLINE=9110524; PubMed=1846440;
 RA Han J., Lu C.-M., Brown G.B., Rado T.A.;
 RT "Direct amplification of a single dissected chromosomal segment by
 RT polymerase chain reaction: a human brain sodium channel gene is on
 RT chromosome 2q22-q23.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
 CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
 CC of excitable membranes. Assuming opened or closed conformations in
 CC response to the voltage difference across the membrane, the
 CC protein forms a sodium-selective channel through which Na(+) ions
 CC may pass in accordance with their electrochemical gradient.
 CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
 CC smaller ones. This sequence represents a large polypeptide.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Adult, 6A;
 CC IsoId=G99250-1; Sequence=displayed;
 CC Name=2; Synonyms=Neonatal, 6N;
 CC IsoId=G99250-2; Sequence=VSP_001032;
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way

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FT REPEAT 1190 1504 III.
FT REPEAT 1513 1811 IV.
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FT TRANSMEM 157 176 S2 of repeat I.
FT TRANSMEM 190 208 S3 of repeat I.
FT TRANSMEM 215 234 S4 of repeat I.
FT TRANSMEM 251 274 S5 of repeat I.
FT TRANSMEM 402 427 S6 of repeat I.
FT TRANSMEM 754 778 S1 of repeat II.
FT TRANSMEM 790 813 S2 of repeat II.
FT TRANSMEM 822 841 S3 of repeat II.
FT TRANSMEM 848 867 S4 of repeat II.
FT TRANSMEM 884 904 S5 of repeat II.
FT TRANSMEM 958 983 S6 of repeat II.
FT TRANSMEM 1204 1227 S1 of repeat III.
FT TRANSMEM 1241 1266 S2 of repeat III.
FT TRANSMEM 1273 1294 S3 of repeat III.
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FT TRANSMEM 1527 1550 S1 of repeat IV.
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FT TRANSMEM 1592 1615 S3 of repeat IV.
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FT CARBOHYD 285 285 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 297 297 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 308 308 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 340 340 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 604 604 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 624 624 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 883 883 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1055 1055 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1072 1072 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1136 1136 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1368 1368 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1382 1382 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1393 1393 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 1778 1778 N-linked (GlcNAc...) (Potential).
FT VARSPPLIC 209 209 D -> N (in Isoform 2).
FT CONFLICT 524 524 /FTId=VSP_001032.
R -> L (in Ref. 1).

Query Match 100.0%; Score 28; DB 1; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7,2e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 YMIFFLVIFLGFIINILAVVAMAY 28
Db 401 YMIFFLVIFLGFIINILAVVAMAY 428

RESULT 5
CIN2_RAT STANDARD; PRT, 2005 AA.
AC P04775;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE subunit).
GN Name=Scn2a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86146901; PubMed=3754035;
RA Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kuraaki M.,
RA Takahashi H., Numa S.;
RT "Existence of distinct sodium channel messenger RNAs in rat brain.",
RL Nature 320:188-192(1986).
CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC of excitable membranes. Assuming opened or closed conformations in
CC response to the voltage difference across the membrane, the
CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC 3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC segment (54). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC or send an email to license@sb-sib.ch.
CC -----
DR EMBL, X03639; CA27287.1; -.
DR PDB, 1BY7; NMR; A=1474-1526.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TripL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IO_region.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR010526; Na_channel_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IO; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS50096; IO; 1.
KW 3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Repeat; Sodium channel; Transmembrane;
KW Voltage-gated channel.
FT REPEAT 111 456 I.
FT REPEAT 741 1013 II.
FT REPEAT 1190 1504 III.
FT REPEAT 1513 1811 IV.
FT TRANSMEM 125 148 S1 of repeat I.
FT TRANSMEM 157 176 S2 of repeat I.
FT TRANSMEM 190 208 S3 of repeat I.
FT TRANSMEM 215 234 S4 of repeat I.
FT TRANSMEM 251 274 S5 of repeat I.
FT TRANSMEM 402 427 S6 of repeat I.
FT TRANSMEM 754 778 S1 of repeat II.
FT TRANSMEM 790 813 S2 of repeat II.
FT TRANSMEM 822 841 S3 of repeat II.
FT TRANSMEM 848 867 S4 of repeat II.
FT TRANSMEM 884 904 S5 of repeat II.
FT TRANSMEM 958 983 S6 of repeat II.
FT TRANSMEM 1204 1227 S1 of repeat III.
FT TRANSMEM 1241 1266 S2 of repeat III.
FT TRANSMEM 1273 1294 S3 of repeat III.
FT TRANSMEM 1320 1340 S4 of repeat III.
FT TRANSMEM 1340 1367 S5 of repeat III.
FT TRANSMEM 1447 1473 S6 of repeat III.
FT TRANSMEM 1527 1550 S1 of repeat IV.
FT TRANSMEM 1562 1585 S2 of repeat IV.
FT TRANSMEM 1592 1615 S3 of repeat IV.

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FT TRANSMEM 1626 1647 S4 of repeat IV.
FT TRANSMEM 1663 1685 S5 of repeat IV.
FT TRANSMEM 1752 1776 S6 of repeat IV.
FT DOMAIN 1905 1934 IO.
FT CARBOHYD 212 212 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 285 285 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 291 291 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 297 297 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 303 303 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 308 308 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 340 340 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 604 604 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 624 624 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 883 883 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1055 1055 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1072 1072 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1136 1136 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1368 1368 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1382 1382 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1393 1393 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 2005 AA; 227872 MW; 861B583D79F8324 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.2e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YMFPLVTFEGSFYINILIAVVMAY 28
Db 401 YMFPLVTFEGSFYINILIAVVMAY 428

RESULT 6
CINI_HUMAN STANDARD; PRT; 2009 AA.
AC P35498; Q16172; Q96LA3; Q9C008;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel protein type I alpha subunit (Voltage-gated sodium channel, alpha subunit Nav1.1) (Sodium channel protein, brain I alpha subunit).
DE GN Name=SCN1A; Synonyms=SCN1, NAC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GEFS+2 MET-875 AND HIS-1648.
RX MEDLINE=20206553; PubMed=10742094;
RA Escayg A., MacDonald B.T., Meisler M.H., Baulac S., Huberfeld G., An-Courfinel I., Brice A., Leguern E., Mouldard B., Chaigne D., Buresi C., Malafosse A.;
RA "Mutations of SCN1A, encoding a neuronal sodium channel, in two families with GEFS+2."
RT Nat. Genet. 24:343-345(2000).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Jeong S.-Y., Goto J., Kanazawa I.;
RT "Cloning of cDNA for human voltage-gated sodium channel alpha subunit, SCN1A."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA Sugawara T., Mazaki E.M., Yamakawa K.;
RT "Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1) mRNA."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT THR-1067.
RA Ouchida M., Omori I.;
RT "Isoforms of human sodium channel SCN1A gene."

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RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1335-1428 FROM N.A.
RX MEDLINE=94340991; PubMed=8062593;
RA Malo M.S., Blanchard B.U., Andresen J.M., Srivastava K., Chen X.N., Li X., Jabe E.W., Korenberg J.R., Ingram V.M.;
RT "Localization of a putative human brain sodium channel gene (SCN1A) to chromosome band 2q24."
RL Cytogenet. Cell Genet. 67:178-186(1994).
RN [6]
RP SEQUENCE OF 1518-1940 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92275082; PubMed=1317301;
RA Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT "Differential expression of two sodium channel subtypes in human brain."
RL FEBS Lett. 303:53-58(1992).
RN [7]
RP VARIANTS GEFS+2 VAL-188; LEU-1353 AND MET-1656.
RX MEDLINE=21152274; PubMed=11254444;
RA Wallace R.H., Scheffer I.E., Barnett S., Richards M., Dibbens L., Desai R.R., Lerman-Segie T., Lev D., Mazarib A., Brand N., Ben-Zeev B., Golkman I., Singh R., Kremidiotis G., Gardner A., Sutherland G.R., George A.L., Jr., Mulley J.C., Berkovic S.F.;
RT "Neuronal sodium-channel alpha1-subunit mutations in generalized epilepsy with febrile seizures plus."
RL Am. J. Hum. Genet. 68:859-865(2001).
RN [8]
RP VARIANTS GEFS+2 ARG-1204.
RX MEDLINE=21152275; PubMed=11254445;
RA Escayg A., Heils A., MacDonald B.T., Haug K., Sander T., Meisler M.H.;
RT "A novel SCN1A mutation associated with generalized epilepsy with febrile seizures plus -- and prevalence of variants in patients with epilepsy."
RL Am. J. Hum. Genet. 68:866-873(2001).
RN [9]
RP VARIANT SMEI PHE-986.
RX MEDLINE=21257503; PubMed=11359211;
RA Claes L., Del-Pavero J., Ceulemans B., Lagae L., Van Broeckhoven C., De Jonghe P.;
RT "De novo mutations in the sodium-channel gene SCN1A cause severe myoclonic epilepsy of infancy."
RL Am. J. Hum. Genet. 68:1327-1332(2001).
RN [10]
RP VARIANTS GEFS+2 THR-1270.
RX MEDLINE=21630138; PubMed=11756608;
RA Abou-Khalil B., Ge Q., Desai R., Ryther R., Bazzyk A., Bailey R., Haines J.L., Sutcliffe J.S., George A.L., Jr.;
RT "Partial and generalized epilepsy with febrile seizures plus and a novel SCN1A mutation."
RL Neurology 57:2265-2272(2001).
RN [1]
RP FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P35498-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P35498-2; Sequence=VSP_001031;
CC Note=No experimental confirmation available;
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.
CC -1- DISEASE: Defects in SCN1A are the cause of generalized epilepsy with febrile seizures plus type 2 (GEFS+2) [MIM:604233]. This

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autosomal dominant disorder is characterized by febrile seizures in children and afebrile seizures in adults. Penetrance is incomplete and a large intrafamilial variability of the phenotype is observed.

-1- DISBASE: Defects in SCN1A are a cause of severe myoclonic epilepsy in infancy (SMEI) [MIM:607208], a severe form of generalized epilepsy with febrile seizures. SMEI is a rare disorder characterized by normal development before onset, seizures beginning in the first year of life in the form of generalized or unilateral febrile clonic seizures, secondary appearance of myoclonic seizures, and occasionally partial seizures. It is associated with ataxia, slowed psychomotor development, and mental decline.

-1- SIMILARITY: Belongs to the sodium channel family.

-1- SIMILARITY: Contains 1 IQ domain.

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DR EMBL; AF25985; AAK0217.1; -
 DR EMBL; AY043484; AAK93560.1; -
 DR EMBL; AB093548; BAC21101.1; -
 DR EMBL; AB093549; BAC21102.1; -
 DR EMBL; S71446; AAB31605.1; -
 DR EMBL; X65362; CAA46439.1; -
 DR EMBL; M91803; -; NOT_ANNOTATED_CDS.
 DR PIR; I52964; I52964.
 DR PIR; S29184; S29184.
 DR HSP; P04775; IBY.
 DR Genew; HGNC:10585; SCN1A.
 DR MIM; 182389; -
 DR MIM; 604233; -
 DR MIM; 607208; -
 DR GO; GO:0016021; C: integral to membrane; NAS.
 DR GO; GO:0005248; P: voltage-gated sodium channel activity; NAS.
 DR GO; GO:0006814; P: sodium ion transport; NAS.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat channel_Tppl.
 DR InterPro; IPR005821; Ca/Na_pore.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR008051; Na_channel1.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans_4.
 DR Pfam; PF00612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc_1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR PRINTS; PRO1664; NACHANNEL1.
 DR PROSITE; PSS0096; IQ; FALSE_NEG.
 KW Alternative splicing; Disease mutation; Epilepsy; Glycoprotein;
 KW Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat;
 KW Sodium channel; Transmembrane; Voltage-gated channel.
 FT REPEAT 110 454
 FT REPEAT 750 1022
 FT REPEAT 1200 1514
 FT REPEAT 1523 1821
 FT TRANSMEM 124 147
 FT TRANSMEM 156 175
 FT TRANSMEM 189 207
 FT TRANSMEM 214 233
 FT TRANSMEM 250 273
 FT TRANSMEM 400 425
 FT TRANSMEM 763 787
 FT TRANSMEM 799 822
 FT TRANSMEM 831 850
 FT TRANSMEM 857 876
 FT TRANSMEM 893 913

FT TRANSMEM 967 992 S6 of repeat II (By similarity).
 FT TRANSMEM 1214 1237 S1 of repeat III (By similarity).
 FT TRANSMEM 1251 1276 S2 of repeat III (By similarity).
 FT TRANSMEM 1283 1304 S3 of repeat III (By similarity).
 FT TRANSMEM 1309 1330 S4 of repeat III (By similarity).
 FT TRANSMEM 1350 1377 S5 of repeat III (By similarity).
 FT TRANSMEM 1457 1483 S6 of repeat III (By similarity).
 FT TRANSMEM 1537 1560 S1 of repeat IV (By similarity).
 FT TRANSMEM 1572 1595 S2 of repeat IV (By similarity).
 FT TRANSMEM 1602 1625 S3 of repeat IV (By similarity).
 FT TRANSMEM 1636 1657 S4 of repeat IV (By similarity).
 FT TRANSMEM 1673 1695 S5 of repeat IV (By similarity).
 FT TRANSMEM 1762 1786 S6 of repeat IV (By similarity).
 FT CARBOHYD 211 211 N-linked (GlcNAc...) (Potential).

Query Match 100.0%; Score 28; DB 1; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 7,2e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YWIFVTVIFGSEFYINLIIAVVAMAY 28
 DB 399 YWIFVTVIFGSEFYINLIIAVVAMAY 426

RESULT 7
 ID CINI_RAT STANDARD; PRT; 2009 AA.
 AC P04774;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel protein type I alpha subunit (voltage-gated sodium channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha subunit).
 DE GN Name=Scn1a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86146901; PubMed=3754035;
 RA Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M., Takahashi H., Numa S.;
 RT "Existence of distinct sodium channel messenger RNAs in rat brain.";
 RL Nature 320:188-192(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87311395; PubMed=2442385;
 RA Noda M., Numa S.;
 RT "Structure and function of sodium channel.";
 RL J. Recept. Res. 7:467-497(1987).
 CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient.
 CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-3 smaller ones. This sequence represents a large polypeptide.
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL, X03638; CAA72986.1; -
CC EMBL, M22253; AAA79965.1; -
DR PIR; A25019; A25019.
DR HSSP; P04775; 1BYX.
DR RGD; 69364; Scn1a.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_Tryp.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR008051; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF005120; Ion_trans_4.
DR Pfam; PF00612; IQ_1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PRINTS; PR01664; NACHANNEL.
DR PROSITE; PS50096; IQ_FALSE_NEG.
KM Glycoprotein; Ion transport; Ionic channel; Multigene family; Repeat;
KW Sodium channel; Transmembrane; Voltage-gated channel.
FT REPEAT 110 454 I.
FT REPEAT 750 1032 II.
FT REPEAT 1200 1514 III.
FT REPEAT 1523 1821 IV.
FT TRANSMEM 124 147 S1 of repeat I.
FT TRANSMEM 156 175 S2 of repeat I.
FT TRANSMEM 189 207 S3 of repeat I.
FT TRANSMEM 214 233 S4 of repeat I.
FT TRANSMEM 250 273 S5 of repeat I.
FT TRANSMEM 400 425 S6 of repeat I.
FT TRANSMEM 763 787 S1 of repeat II.
FT TRANSMEM 799 822 S2 of repeat II.
FT TRANSMEM 831 850 S3 of repeat II.
FT TRANSMEM 857 876 S4 of repeat II.
FT TRANSMEM 883 913 S5 of repeat II.
FT TRANSMEM 967 992 S6 of repeat II.
FT TRANSMEM 1214 1237 S1 of repeat III.
FT TRANSMEM 1251 1276 S2 of repeat III.
FT TRANSMEM 1283 1304 S3 of repeat III.
FT TRANSMEM 1309 1330 S4 of repeat III.
FT TRANSMEM 1350 1377 S5 of repeat III.
FT TRANSMEM 1457 1483 S6 of repeat III.
FT TRANSMEM 1537 1560 S1 of repeat IV.
FT TRANSMEM 1572 1595 S2 of repeat IV.
FT TRANSMEM 1602 1625 S3 of repeat IV.
FT TRANSMEM 1636 1657 S4 of repeat IV.
FT TRANSMEM 1673 1695 S5 of repeat IV.
FT TRANSMEM 1762 1786 S6 of repeat IV.
FT CARBOHYD 211 211 N-1-linked (GlcNAc...)
FT CARBOHYD 284 284 N-1-linked (GlcNAc...)
FT CARBOHYD 295 295 N-1-linked (GlcNAc...)
FT CARBOHYD 301 301 N-1-linked (GlcNAc...)
FT CARBOHYD 306 306 N-1-linked (GlcNAc...)
FT CARBOHYD 338 338 N-1-linked (GlcNAc...)
FT CARBOHYD 601 601 N-1-linked (GlcNAc...)
FT CARBOHYD 621 621 N-1-linked (GlcNAc...)
FT CARBOHYD 681 681 N-1-linked (GlcNAc...)
FT CARBOHYD 892 892 N-1-linked (GlcNAc...)
FT CARBOHYD 1060 1060 N-1-linked (GlcNAc...)
FT CARBOHYD 1064 1064 N-1-linked (GlcNAc...)
FT CARBOHYD 1080 1080 N-1-linked (GlcNAc...)
FT CARBOHYD 1146 1146 N-1-linked (GlcNAc...)
FT CARBOHYD 1378 1378 N-1-linked (GlcNAc...)
FT CARBOHYD 1392 1392 N-1-linked (GlcNAc...)
FT CARBOHYD 1403 1403 N-1-linked (GlcNAc...)
SQ SEQUENCE 2009 AA; 228769 MW; 6808466f636837B CRC64;

Query Match 100.0%; Score 28; DB 1; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.2e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMIFFVLVIFLGSFYILNITLAVVMAY 28
Db 399 YMIFFVLVIFLGSFYILNITLAVVMAY 426

RESULT 8
042419 PRELIMINARY; PRT; 213 AA.
ID 042419
AC 042419; PRELIMINARY; PRT; 213 AA.
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Voltage-gated sodium channel I (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dorsal root ganglion;
RX MEDLINE=98024190; PubMed=9356508;
RA Friedel R.H., Schnuerch H., Stubbusch J., Barde Y.A.;
RT "Identification of genes differentially expressed by nerve growth factor- and neurotrophin-3-dependent sensory neurons".
RL Proc. Natl. Acad. Sci. U.S.A. 94:12670-12675(1997).
DR EMBL; AJ001489; CAA04784.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1 213
FT NON_TER 1 213
SQ SEQUENCE 213 AA; 24397 MW; DAF3B6AE4E8B47ED CRC64;

Query Match 75.0%; Score 21; DB 2; Length 213;
Best Local Similarity 100.0%; Pred. No. 5.7e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMIFFVLVIFLGSFYILNITL 21
Db 193 YMIFFVLVIFLGSFYILNITL 213

RESULT 9
042420 PRELIMINARY; PRT; 225 AA.
ID 042420
AC 042420; PRELIMINARY; PRT; 225 AA.
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Voltage-gated sodium channel II (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dorsal root ganglion;
RX MEDLINE=98024190; PubMed=9356508;
RA Friedel R.H., Schnuerch H., Stubbusch J., Barde Y.A.;
RT "Identification of genes differentially expressed by nerve growth factor- and neurotrophin-3-dependent sensory neurons".
RL Proc. Natl. Acad. Sci. U.S.A. 94:12670-12675(1997).
DR EMBL; AJ001490; CAA04785.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.

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DR GO: GO:0005261; F: cation channel activity; IEA.
DR GO: GO:0006812; P: cation transport; IEA.
DR InterPro: IPR001682; Ca/Na pore.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR005820; M+channel_nlg.
DR Pfam: PF00520; Ion_trans_1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON TER 1 225
SQ SEQUENCE 225 AA; 25531 MW; 85B122E582F3023E CRC64;

Query Match 75.0%; Score 21; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.9e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMFPLVIFLGSFYINLIL 21
DB 205 YMFPLVIFLGSFYINLIL 225

RESULT 10
Q9IBD6 PRELIMINARY; PRT; 247 AA.
AC Q9IBD6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Skeletal muscle voltage-gated sodium channel (Fmna2) (Fragment).
OS Takifugu pardalis (Pufferfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
RX NCBI_TaxID=98921;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=20090650; PubMed=10623632;
RA Yocsu-Yamashita M., Nishimori K., Nitanai Y., Isejima M., Sugimoto A.,
RA Yaumoto T.;
RT "Binding properties of 3H-PbTx-3 and 3H-saxitoxin to brain membranes
RT and to skeletal muscle membranes of puffer fish Takifugu pardalis, and the
RT primary structure of a voltage-gated Na+ channel alpha-subunit (Fmna1)
RT from skeletal muscle of F. pardalis."
RL Biochem. Biophys. Res. Commun. 267:403-412 (2000).
DR EMBL: AB032022; BAA90308.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005261; P: cation channel activity; IEA.
DR GO: GO:0006812; P: cation transport; IEA.
DR InterPro: IPR001682; Ca/Na_pore.
DR InterPro: IPR005821; Ion_trans.
DR InterPro: IPR005820; M+channel_nlg.
DR Pfam: PF00520; Ion_trans_1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON TER 1 247
SQ SEQUENCE 247 AA; 27998 MW; 0B8C1CECF05E1F5 CRC64;

Query Match 75.0%; Score 21; DB 2; Length 247;
Best Local Similarity 100.0%; Pred. No. 6.4e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VIFLGSFYINLILVVMAY 28
DB 223 VIFLGSFYINLILVVMAY 243

RESULT 11
ID CINA_ELEBL STANDARD; PRT; 1820 AA.
AC P02719;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Sodium channel protein (Na+) channel.
OS Electrophorus electricus (Electric eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC Electrophoridae; Electrophorus.
RX NCBI_TaxID=8005;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85061498; PubMed=6209577;
RA Noda M., Shimizu S., Tanabe T., Takai T., Kayano T., Ikeda T.,
RA Takahashi H., Nakayama H., Kanaoka Y., Minamino N., Kangawa K.,
RA Matsuo H., Kaitery M.A., Hirose T., Inayama S., Hayashida H.,
RA Miyata T., Numa S.;
RT "Primary structure of Electrophorus electricus sodium channel deduced
RT from cDNA sequence."
RL Nature 312:121-127 (1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87311395; PubMed=2442385;
RA Noda M., Numa S.;
RT "Structure and function of sodium channel."
RL J. Recept. Res. 7:467-497 (1987).
CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC of excitable membranes. Assuming opened or closed conformations in
CC response to the voltage difference across the membrane, the
CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- MISCELLANEOUS: Available data suggest that activation and
CC inactivation gates are located near the cytoplasmic surface of the
CC membrane. It is hypothesized that residues 802-806, 847-857, 894-
CC 910, and 942-955 might, in conjunction with the positively charged
CC residues of S4, act as a voltage sensor involved with the
CC activation gate.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X01119; CAA25587.1; -.
DR EMBL: M22252; AAA79960.1; -.
DR PIR: A01378; CHEE.
DR HSSP: P04775; IBY.
DR InterPro: IPR001682; Ca/Na_pore.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR005821; Ion_trans.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR005820; M+channel_nlg.
DR InterPro: IPR001686; Na_channel.
DR Pfam: PF00520; Ion_trans_1.
DR Pfam: PF00520; Ion_trans_4.
DR Pfam: PF06512; Na_trans_assoc_1.
DR PRINTS: PR00170; NACHTANL.
DR PROSITE: PS50096; IQ_FALSR_NEG.
KW Glycoprotein; Ion transport; Ionic channel; Repeat; Sodium channel;
KW Transmembrane; Voltage-gated channel.
FT REPEAT 111 419 1.
FT REPEAT 555 807 II.
FT REPEAT 989 1281 III.
FT REPEAT 1311 1587 IV.

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FT TRANSMEM 118 138 S1 of repeat I.
FT TRANSMEM 150 171 S2 of repeat I.
FT TRANSMEM 177 197 S3 of repeat I.
FT TRANSMEM 204 224 S4 of repeat I.
FT TRANSMEM 244 264 S5 of repeat I.
FT TRANSMEM 285 342 Non-homologous region of repeat I.
FT TRANSMEM 379 402 S6 of repeat I.
FT TRANSMEM 558 578 S1 of repeat II.
FT TRANSMEM 600 620 S2 of repeat II.
FT TRANSMEM 626 643 S3 of repeat II.
FT TRANSMEM 651 671 S4 of repeat II.
FT TRANSMEM 691 711 S5 of repeat II.
FT TRANSMEM 767 790 S6 of repeat II.
FT TRANSMEM 1005 1025 S1 of repeat III.
FT TRANSMEM 1038 1058 S2 of repeat III.
FT TRANSMEM 1066 1086 S3 of repeat III.
FT TRANSMEM 1092 1112 S4 of repeat III.
FT TRANSMEM 1132 1152 S5 of repeat III.
FT TRANSMEM 1172 1194 Non-homologous region of repeat III.
FT TRANSMEM 1244 1264 S6 of repeat III.
FT TRANSMEM 1321 1341 S1 of repeat IV.
FT TRANSMEM 1353 1376 S2 of repeat IV.
FT TRANSMEM 1381 1398 S3 of repeat IV.
FT TRANSMEM 1417 1437 S4 of repeat IV.
FT TRANSMEM 1454 1474 S5 of repeat IV.
FT TRANSMEM 1490 1505 Non-homologous region of repeat IV.
FT TRANSMEM 1544 1567 S6 of repeat IV.
FT CAROXYD 278 278 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 288 288 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 317 317 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 591 591 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 630 630 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 797 797 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 1160 1160 N-linked (GlcNAc. . .) (Potential).
FT CAROXYD 1174 1174 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 1820 AA; 208331 MW; 1B271F626E057864 CRC64;

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Query Match 75.0%; Score 21; DB 1; Length 1820;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VFLLSFFYLINILAVVMAY 28
 |||||
 Db 385 VFLLSFFYLINILAVVMAY 405

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RESULT 12
Q1BFL PRELIMINARY; PRT; 1880 AA.
AC Q1BFL:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Voltage-gated sodium channel.
OS Takifugu pardalis (Panther puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=98921;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=20090550; PubMed=10623632;
RA Yotau-Yamashita M., Nishimori K., Nitanai Y., Iseura M., Sugimoto A.,
RA Yasumoto T.;
RT "Binding properties of 3H-PBTx-3 and 3H-saxitoxin to brain membranes
RT and to skeletal muscle membranes of puffer fish Takifugu pardalis, and the
RT primary structure of a voltage-gated Na+ channel alpha-subunit (fMaai)
RT from skeletal muscle of F. pardalis."
RL Biochem. Biophys. Res. Commun. 267:403-412(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.

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DR EMBL; AB030482; BAA90398.1; -.
DR HSSP; P04775; 1BYX.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; C:ion channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:ion channel transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel1.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF0612; IQ_1.
DR Pfam; PF06512; Na_trans_assoc_1.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS50096; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1880 AA; 212084 MW; 406483C6C3D43E02 CRC64;

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Query Match 75.0%; Score 21; DB 2; Length 1880;
 Best Local Similarity 100.0%; Pred. No. 2.9e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VFLLSFFYLINILAVVMAY 28
 |||||
 Db 405 VFLLSFFYLINILAVVMAY 425

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RESULT 13
Q1S858 PRELIMINARY; PRT; 1977 AA.
AC Q1S858;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Sodium channel alpha subunit.
GN Name=hmr-Na;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RX MEDLINE=95237189; PubMed=7720699;
RA Klugbauer N., Lacinova L., Flockeiz V., Hofmann F.;
RT "Structure and functional expression of a new member of the
RT tetrodotoxin-sensitive voltage-activated sodium channel family from
RT human neuroendocrine cells."
RL EMBO J. 14:1084-1090(1995).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; X82835; CAAS8042.1; -.
DR PIR; S54771; S54771.
DR HSSP; P04775; 1BYX.
DR Genew; HGNC:10597; SCN9A.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR GO; GO:0006814; P:sodium ion transport; TAS.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel1.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF0612; IQ_1.
DR Pfam; PF06512; Na_trans_assoc_1.

```

DR PRINTS; PR00170; NACHANNEL.
 DR SMART; SM00015; IQ; 1.
 DR Ion transport; Ionic channel; Sodium channel; Transmembrane;
 DR Transport; Voltage-gated channel.
 SQ SEQUENCE 1977 AA; 225195 MW; 17D67BC32BC15FB CRC64;

Query Match 75.0%; Score 21; DB 2; Length 1977;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VIFGSPYILNLIIVAVMAY 28
 |||||
 DB 385 VIFGSPYILNLIIVAVMAY 405

RESULT 14
 Q28644 PRELIMINARY; PRT; 1984 AA.
 AC Q28644;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Sodium channel alpha-subunit.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RX NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand White; TISSUE=Sciatic nerve;
 RX MEDLINE=96074641; PubMed=7479931;
 RA Belcher S.M., Zerial C.A., Levenson R., Ritchie J.M., Howe J.R.;
 RT "Cloning of a sodium channel alpha subunit from rabbit Schwann
 cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; U35238; AAA89159.1; -.
 DR HSSP; P04775; 1BYV.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005248; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans_4.
 DR Pfam; PF00612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR SMART; SM00015; IQ; 1.
 DR Ion transport; Ionic channel; Sodium channel; Transmembrane;
 DR Transport; Voltage-gated channel.
 SQ SEQUENCE 1984 AA; 225748 MW; 98F76860C9866AA0 CRC64;

Query Match 75.0%; Score 21; DB 2; Length 1984;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VIFGSPYILNLIIVAVMAY 28
 |||||
 DB 383 VIFGSPYILNLIIVAVMAY 403

RESULT 15
 008562 PRELIMINARY; PRT; 1984 AA.
 ID 008562

AC 008562;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE PNI (Voltage-gated sodium channel) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97188502; PubMed=9037087;
 RA Toledo-Aral J.J., Moss B.L., He Z.J., Koszowski A.G., Whisenand T.,
 RA Levinson S.R., Wolf J.J., Silos-Santiago I., Halsegou S., Mandel G.;
 RT "Identification of PNI, a predominant voltage-dependent sodium channel
 expressed principally in peripheral neurons.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:1527-1532(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97007982; PubMed=8854872;
 RA Kozak C.A., Sangameswaran L.;
 RT "Genetic mapping of the peripheral sodium channel genes, Scn5a and
 Scn10a, in the mouse.";
 RL Mamm. Genome 7:787-788(1996).
 RN [3]

RP SEQUENCE FROM N.A.
 RA Sangameswaran L., Fish L.M., Koch B.D., Rabert D.K., Delgado S.G.,
 RA Ilinicka M., Jakeman L.B., Novakovic S., Wong K., Sze P., Tzounakia E.,
 RA Stewart G.R., Herman R.C., Chan H., Eglén R.M., Hunter J.C.;
 RT "A novel tetrodotoxin-sensitive, voltage-gated sodium channel
 expressed in rat and human dorsal root ganglia.";
 RL J. Biol. Chem. 272:13977-13982(1997).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; U79568; AAB50403.1; -.
 DR EMBL; AF000368; AAB80701.1; -.
 DR HSSP; P04775; 1BYV.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans_4.
 DR Pfam; PF00612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR SMART; SM00015; IQ; 1.
 DR Ion transport; Ionic channel; Sodium channel; Transmembrane;
 DR Transport; Voltage-gated channel.
 FT NON_TER 1984
 SQ SEQUENCE 1984 AA; 226037 MW; 386C38B9B5097091 CRC64;

Query Match 75.0%; Score 21; DB 2; Length 1984;
 Best Local Similarity 100.0%; Pred. No. 3.1e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VIFGSPYILNLIIVAVMAY 28
 |||||
 DB 385 VIFGSPYILNLIIVAVMAY 405

RESULT 16
 025150 PRELIMINARY; PRT; 2049 AA.
 AC 025150;

DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Voltage-gated sodium channel.
 GN Name=tunat;
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
 OC Stolidobranchia; Pyrosidae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95033215; PubMed=7946338;
 RA Okamura Y., Ono F., Okagaki R., Chong J., Mandel G.;
 RT "Neural expression of a sodium channel gene requires cell-specific
 interactions";
 RL Neuron 13:937-948(1994).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL, D17311; BAA04133.1; -.
 DR PIR, T43161; T43161.
 DR HSSP; P04775; 1BYV.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na_Pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M_channel_nlg.
 DR InterPro; IPR001696; Na_channel_nlg.
 DR Pfam; PF00520; Ion_trans_4.
 DR Pfam; PF00612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR SMART; SM00015; IQ_1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 2049 AA; 233443 MW; F7DE3578105B73PB CRC64;
 Query Match 75.0%; Score 21; DB 2; Length 2049;
 Best Local Similarity 100.0%; Fred NO. 3.1e-11;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 VIFLGSFYILNILLAVVMAY 28
 |||||
 DB 449 VIFLGSFYILNILLAVVMAY 469

RESULT 17
 CIN4_HUMAN STANDARD; PRT; 1836 AA.
 ID P35459; O15478; Q16447; Q726B1;
 AC P35459; O15478; Q16447; Q726B1;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel protein type IV alpha subunit (Voltage-gated sodium
 DE channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle
 DE alpha-subunit).
 GN Name=SCN4A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT ASP-559.
 RX TISSUE=Skeletal muscle;
 RX MEDLINE=92246457; PubMed=1315496;
 RA George A.L., Jr., Komisarof J., Kallen R.G., Barchi R.L.;
 RT "Primary structure of the adult human skeletal muscle voltage-

RT dependent sodium channel.";
 RL Ann. Neurol. 31:131-137(1992).
 RN [2].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92134303; PubMed=1310396;
 RA Wang J., Rojas C.V., Zhou J., Schwartz L.S., Nicholas H.,
 RA Hoffmann E.P.;
 RT "Sequence and genomic structure of the human adult skeletal muscle
 RT sodium channel alpha subunit gene on 17q.";
 RL Biochem. Biophys. Res. Commun. 182:794-801(1992).
 RN [3]
 RP SEQUENCE FROM N.A., VARIANT MYASTHENIC SYNDROME GLU-1442, AND VARIANTS
 RP LEU-246, ASP-559 AND ASN-1376.
 RX MEDLINE=22684480; PubMed=12766226; DOI=10.1073/pnas.1230273100;
 RA Teujino A., Maertens C., Ono K., Shen X.-M., Fukuda T., Harper C.M.,
 RA Cannon S.C., Engel A.G.;
 RT "Myasthenic syndrome caused by mutation of the SCN4A sodium channel.";
 RT Proc. Natl. Acad. Sci. U.S.A. 100:7377-7382(2003).
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANT ASN-1376.
 RX MEDLINE=9338444; PubMed=1339144;
 RA McClatchey A.I., Lin C.S., Wang J., Hoffman E.P., Rojas C.V.,
 RA Guseella J.F.;
 RT "The genomic structure of the human skeletal muscle sodium channel
 RT gene.";
 RL Hum. Mol. Genet. 1:521-521(1992).
 RN [5]
 RP SEQUENCE OF 1305-1339 FROM N.A., AND VARIANTS PMC VAL-1306 AND
 RP MET-1313.
 RX MEDLINE=92154689; PubMed=1310898;
 RA McClatchey A.I., van den Berg P., Pericak-Vance M.A., Raekind W.,
 RA Verellen C., McKenna-Yasek D., Rao K., Haines J.L., Bird T.,
 RA Brown R.H., Jr., Guseella J.F.;
 RT "Temperature-sensitive mutations in the III-IV cytoplasmic loop region
 RT of the skeletal muscle sodium channel gene in paramyotonia
 RT congenita.";
 RL Cell 68:769-774(1992).
 RN [6]
 RP VARIANT HYP MET-704.
 RX MEDLINE=92069747; PubMed=1659948;
 RA Ptacek L.J., George A.L., Jr., Griggs R.C., Tawil R., Kallen R.G.,
 RA Barchi R.L., Robertson M., Leppert M.F.;
 RT "Identification of a mutation in the gene causing hyperkalemic
 RT periodic paralysis.";
 RL Cell 67:1021-1027(1991).
 RN [7]
 RP VARIANT HYP VAL-1592.
 RX MEDLINE=92065978; PubMed=1659668;
 RA Rojas C.V., Wang J., Schwartz L.S., Hoffman E.P., Powell B.R.,
 RA Brown R.H., Jr.;
 RT "A Met-to-Val mutation in the skeletal muscle Na+ channel alpha-
 RT subunit in hyperkalemic periodic paralysis.";
 RL Nature 354:387-389(1991).
 RN [8]
 RP VARIANTS PMC PHE-804 AND THR-1156.
 RX MEDLINE=93265141; PubMed=1338909;
 RA McClatchey A.I., McKenna-Yasek D., Cros D., Worthen H.G., Kuncel R.W.,
 RA Desilva S.M., Corbiath D.R., Guseella J.F., Brown R.H., Jr.;
 RT "Novel mutations in families with unusual and variable disorders of
 RT the skeletal muscle sodium channel.";
 RL Nat. Genet. 2:148-152(1992).
 RN [9]
 RP VARIANTS PMC CYS-1448 AND HIS-1448.
 RX MEDLINE=92265302; PubMed=1316765;
 RA Ptacek L.J., George A.L., Jr., Barchi R.L., Griggs R.C., Riggs J.E.,
 RA Robertson M., Leppert M.F.;
 RT "Mutations in an S4 segment of the adult skeletal muscle sodium
 RT channel cause paramyotonia congenita.";
 RL Neuron 8:891-897(1992).
 RN [10]
 RP VARIANT PMC ARG-1433.
 RX MEDLINE=93270429; PubMed=8388676;
 RA Ptacek L.J., Gow L., Kwiecinski H., McManis P., Mendell J.R.,

RA Barohn R.J., George A.L. Jr., Barchi R.L., Robertson M., Leppert M.F.;
 RT "Sodium channel mutations in paramyotonia congenita and hyperkalemic
 RT periodic paralysis.";
 RL Ann. Neurol. 33:300-307(1993).
 RN [11]
 RP VARIANTS PMC ALA-1306, GLU-1306 AND VAL-1306.
 RX MEDLINE=94141728; PubMed=8308722;
 RA Lerche H., Heine R., Pika U., George A.L. Jr., Mitrivic N.,
 RA Bratzki M., Weiss T., Rivet-Bastide M., Franke C., Lomomaco M.,
 RA Ricker K., Lehmann-Horn F.;
 RT "Human sodium channel myotonia: slowed channel inactivation due to
 RT substitutions for a glycine within the III-IV linker.";
 RL J. Physiol. (Lond.) 470:13-22(1993).
 RN [12]
 RP VARIANT PMC MET-1589.
 RX MEDLINE=94061027; PubMed=8242056;
 RA Heine R., Pika U., Lehmann-Horn F.;
 RT "A novel SCN4A mutation causing myotonia aggravated by cold and
 RT potassium.";
 RL Hum. Mol. Genet. 2:1349-1353(1993).
 RN [13]
 RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA VAL-1160.
 RX PubMed=8058156;
 RA Ptacek L.J., Tawil R., Grigge R.C., Meola G., McManis P., Barohn R.J.,
 RA Mendell J.R., Harris C., Spitzer R., Santiago F., Leppert M.F.;
 RT "Sodium channel mutations in acetazolamide-responsive myotonia
 RT congenita, paramyotonia congenita, and hyperkalemic periodic
 RT paralysis.";
 RL Neurology 44:1500-1503(1994).
 RN [14]
 RP VARIANT PARAMYOTONIA WITHOUT COLD PARALYSIS ILE-1293.
 RX MEDLINE=96154961; PubMed=8580427;
 RA Koch M.C., Baumbach K., George A.L., Ricker K.;
 RT "Paramyotonia congenita without paralysis on exposure to cold: a novel
 RT mutation in the SCN4A gene (Val1293Ile).";
 RL NeuroReport 6:2001-2004(1995).
 RN [15]
 RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA MET-445.
 RX PubMed=9392583;
 RA Rosenfeld J., Sloan-Brown K., George A.L. Jr.;
 RT "A novel muscle sodium channel mutation causes painful congenital
 RT myotonia.";
 RL Ann. Neurol. 42:811-814(1997).
 RN [16]
 RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA MET-445.
 RX PubMed=10218481;
 RA Wang D.W., Vanhegarr D., Ruben P.C., George A.L. Jr., Bennett P.B.;
 RT "Functional consequences of a domain I/S6 segment sodium channel
 RT mutation associated with painful congenital myotonia.";
 RL FEBS Lett. 448:231-234(1999).
 RN [17]
 RP VARIANT HYPOKPP HIS-669.
 RX PubMed=10599760;
 RA Bulman D.E., Scoggan K.A., van Oene M.D., Nicolle M.W., Hahn A.F.,
 RA Toller L.L., Ebers G.C.;
 RT "A novel sodium channel mutation in a family with hypokalemic periodic
 RT paralysis.";
 RL Neurology 53:1932-1936(1999).
 RN [18]
 RP VARIANT HYPOKPP SER-1158.
 RX PubMed=10851391;
 RA Sugita Y., Aoki T., Sugiyama Y., Hida C., Ogata M., Yamamoto T.;
 RT "Temperature-sensitive sodium channelopathy with heat-induced myotonia
 RT and cold-induced paralysis.";
 RL Neurology 54:2179-2181(2000).
 RN [19]
 RP VARIANTS HYPOKPP GLY-672 AND HIS-672.
 RX PubMed=10944223;
 RA Jurkat-Rott K., Mitrivic N., Hang C., Kouzmekine A., Ializzo P.,
 RA Herzog J., Lerche H., Nicole S., Vale-Santos J., Chauveau D.,
 RA Fontaine B., Lehmann-Horn F.;
 RT "Voltage-sensor sodium channel mutations cause hypokalemic periodic
 RT paralysis type 2 by enhanced inactivation and reduced current.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:9549-9554(2000).
 RN [20]
 RP VARIANT HYPOKPP SER-672.
 RX PubMed=11558801;
 RA Bendahhou S., Cummins T.R., Grigge R.C., Fu Y.H., Ptacek L.J.;
 RT "Sodium channel inactivation defects are associated with
 RT acetazolamide-exacerbated hypokalemic periodic paralysis.";
 RL Ann. Neurol. 50:417-420(2001).
 RN [21]
 RP VARIANT HYPOKPP SER-672.
 RX PubMed=11591859;
 RA Davies N.P., Runson L.H., Samuel M., Hanna M.G.;
 RT "Sodium channel gene mutations in hypokalemic periodic paralysis: an
 RT uncommon cause in the UK.";
 RL Neurology 57:1323-1325(2001).
 CC -1- FUNCTION: This protein mediates the voltage-dependent sodium ion
 CC permeability of excitable membranes. Assuming opened or closed
 CC membrane, the protein forms a sodium-selective channel through
 CC which Na+ ions may pass in accordance with their electrochemical
 CC gradient. This sodium channel may be present in both denervated
 CC and innervated skeletal muscle.
 CC -1- SUBUNIT: Muscle sodium channels contain an alpha subunit and a
 CC smaller beta subunit. Interacts with the PDZ domain of the
 CC synaptrophin SNTA1, SNTA1 and SNTB2 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- DISEASE: Defects in SCN4A are the cause of paramyotonia congenita
 CC of von Erlenburg (PMC) [MIM:168300]. PMC is an autosomal dominant
 CC sodium channel disease characterized by myotonia, increased by
 CC exposure to cold, intermittent flaccid paresthesia, not necessarily

Query Match 71.4%; Score 20; DB 1; Length 1836;
 Best Local Similarity 100.0%; Pred. No. 2.6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 9 IFGSPFLNLIIVAVMAY 28
 Db 431 IFGSPFLNLIIVAVMAY 450

RESULT 18
 CIN4_RAT
 ID CIN4_RAT STANDARD; PRT; 1840 AA.
 AC P15390;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel protein type IV alpha subunit (Voltage-gated sodium
 DE channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle
 DE alpha-subunit) (Mn-1).
 GN Name=Scn4a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148778; PubMed=2559760;
 RA Trimmer J.S., Cooperman S.S., Tomko S.A., Zhou J., Crean S.M.,
 RA Boyle M.B., Kallen R.G., Sheng Z., Barchi R.L., Sigworth F.J.,
 RA Goodman R.H., Agnew W.S., Mandel G.;
 RT "Primary structure and functional expression of a mammalian skeletal
 RT muscle sodium channel.";
 RL Neuron 3:33-49(1989).
 CC -1- FUNCTION: This protein mediates the voltage-dependent sodium ion
 CC permeability of excitable membranes. Assuming opened or closed
 CC conformations in response to the voltage difference across the
 CC membrane, the protein forms a sodium-selective channel through

CC which Na+ ions may pass in accordance with their electrochemical
 CC gradient. This sodium channel may be present in both denervated
 CC and innervated skeletal muscle.
 CC -1- SUBUNIT: Muscle sodium channels contain an alpha subunit and a
 CC smaller beta subunit. Interacts with the PDZ domain of the
 CC syntrophin SYNT1, SYNT1 and SYNT2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, M26643; AAA41682.1; -
 CC PIR, J00007; CHRTM1.
 CC HSSP, P04775; IBYV.
 CC InterPro: IPR001582; Ca/Na_pore.
 CC InterPro: IPR002111; Cat_channel_TrpL.
 CC InterPro: IPR005821; Ion_trans.
 CC InterPro: IPR000048; IQ_region.
 CC InterPro: IPR005820; M-channel_nlg.
 CC InterPro: IPR001696; Na_channel.
 CC InterPro: IPR008052; Na_channel4.
 CC InterPro: IPR010526; Na_trans_assoc.
 CC Pfam: PF00520; Ion_trans; 4.
 CC Pfam: PF06512; IQ; 1.
 CC Pfam: PF06512; Na_trans_assoc; 1.
 CC PRINTS: PR00170; NACHANNEL.
 CC PROSITE: PS50096; IQ; 1.
 CC Glycoprotein; Ion transport; Ionic channel; Multigene family;
 CC Phosphorylation; Repeat; Sodium channel; Transmembrane;
 CC Voltage-gated channel.
 CC TRANSMEM 130 152 S1 of repeat I.
 CC TRANSMEM 156 179 S2 of repeat I.
 CC TRANSMEM 192 212 S3 of repeat I.
 CC TRANSMEM 214 233 S4 of repeat I.
 CC TRANSMEM 252 274 S5 of repeat I.
 CC TRANSMEM 417 444 S6 of repeat I.
 CC TRANSMEM 571 593 S1 of repeat II.
 CC TRANSMEM 663 685 S2 of repeat II.
 CC TRANSMEM 696 721 S3 of repeat II.
 CC TRANSMEM 722 737 S4 of repeat II.
 CC TRANSMEM 756 778 S5 of repeat II.
 CC TRANSMEM 832 859 S6 of repeat II.
 CC TRANSMEM 1084 1105 S1 of repeat III.
 CC TRANSMEM 1117 1140 S2 of repeat III.
 CC TRANSMEM 1149 1168 S3 of repeat III.
 CC TRANSMEM 1176 1195 S4 of repeat III.
 CC TRANSMEM 1215 1236 S5 of repeat III.
 CC TRANSMEM 1324 1351 S6 of repeat III.
 CC TRANSMEM 1405 1427 S1 of repeat IV.
 CC TRANSMEM 1437 1460 S2 of repeat IV.
 CC TRANSMEM 1468 1487 S3 of repeat IV.
 CC TRANSMEM 1502 1522 S4 of repeat IV.
 CC TRANSMEM 1535 1556 S5 of repeat IV.
 CC TRANSMEM 1627 1653 S6 of repeat IV.
 CC DOMAIN 1720 1749 IQ.
 CC CARBOHYD 268 288 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 291 297 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 297 297 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).
 CC CARBOHYD 309 309 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 315 315 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 327 327 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 356 356 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 502 502 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 954 954 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1198 1198 N-linked (GlcNAc...) (Potential).
 FT MOD_RES 251 251 Phosphoserine (by PKA) (Potential).
 FT MOD_RES 1321 1321 Phosphoserine (by PKA) (Potential).
 FT MOD_RES 1504 1504 Phosphoserine (by PKA) (Potential).
 SQ SEQUENCE 1840 AA; 208865 MW; CSDC09D93DD9FAD6 CRC64;
 Query Match 71.4%; Score 20; DB 1; Length 1840;
 Best Local Similarity 100.0%; Pred. No. 2,6e-10;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 IFLGSFYILNLLAVVAVMAY 28
 DB 425 IFLGSFYILNLLAVVAVMAY 444
 RESULT 19
 ID 070611 PRELIMINARY; PRT; 1840 AA.
 AC 070611;
 DT 01-AUG-1998 (TRMBLrel. 07, Created)
 DT 01-AUG-1998 (TRMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
 DE Rat skeletal muscle type I voltage-gated sodium channel (RSMX1)
 DE variant.
 GN Name=SCN4A;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Copenhagen; TISSUE=Prostate;
 RX MEDLINE=96273645; PubMed=9613589;
 RA Dis J.K.J., Stewart D., Fraser S.P., Black J.A., Dibb-Hajj S.,
 RA Waxman S.G., Archer S.N., Djamgoz M.B.A.;
 RT "Expression of skeletal muscle-type voltage-gated Na+ channel in rat
 RT and human prostate cancer cell lines.";
 RL FEBS Lett. 427:5-10(1998).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC EMBL, Y17153; CA76659.1; -
 CC HSSP, P04775; IBYV.
 CC GO: GO:0016021; C:Integral to membrane; IEA.
 CC GO: GO:0005261; F:cation channel activity; IEA.
 CC GO: GO:0005246; F:voltage-gated sodium channel activity; IEA.
 CC GO: GO:0006812; P:cation transport; IEA.
 CC GO: GO:0006814; P:sodium ion transport; IEA.
 CC InterPro: IPR001682; Ca/Na_pore.
 CC InterPro: IPR002111; Cat_channel_TrpL.
 CC InterPro: IPR005821; Ion_trans.
 CC InterPro: IPR000048; IQ_region.
 CC InterPro: IPR005820; M-channel_nlg.
 CC InterPro: IPR001696; Na_channel.
 CC InterPro: IPR008052; Na_channel4.
 CC InterPro: IPR010526; Na_trans_assoc.
 CC Pfam: PF00520; Ion_trans; 4.
 CC Pfam: PF06512; IQ; 1.
 CC Pfam: PF06512; Na_trans_assoc; 1.
 CC PRINTS: PR00170; NACHANNEL.
 CC SMART: SM00015; IQ; 1.
 CC PROSITE: PS50096; IQ; 1.
 CC Ion transport; Ionic channel; Sodium channel; Transmembrane;
 CC Transport; Voltage-gated channel.
 SQ SEQUENCE 1840 AA; 208823 MW; BIDFFAS38E264B40 CRC64;

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Query Match      71.4%; Score 20; DB 2; Length 1840;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFLGSYFLINLILAVVAVVAY 28
DB 425 IFLGSYFLINLILAVVAVVAY 444

RESULT 20
Q9ER60 PRELIMINARY; PRT; 1841 AA.
AC Q9ER60;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Voltage-gated sodium channel.
GN Name=Scn4a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=balb/c; TISSUE=Heart;
RX MEDLINE=21823196; PubMed=11834493;
RA Zimmer T., Benndorf K.;
RT "The mouse heart sodium channel (mH1): cloning and characterization of
RT alternatively spliced variants."
RL Am. J. Physiol. Heart Circ. Physiol. 282:HI007-HI017(2002).
CC -1 SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; A3278787; CACCT7146.1; -.
DR HSSP; P04775; IBY.
DR MGD; MGI:98250; Scn4a.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat channel_Tppl.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001686; Na_channel.
DR InterPro; IPR008052; Na_channel14.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF00612; IQ_1.
DR Pfam; PF06512; Na_trans_assoc_1.
DR PRINTS; PRO0170; NACHANNEL.
DR PRINTS; PRO1665; NACHANNEL4.
DR SMART; SM00015; IQ_1.
DR PROSITE; PSS0096; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1841 AA; 208796 MW; 0766DFD33A9E0B55 CRC64;

Query Match      71.4%; Score 20; DB 2; Length 1841;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFLGSYFLINLILAVVAVVAY 28
DB 425 IFLGSYFLINLILAVVAVVAY 444

RESULT 21
Q90518 PRELIMINARY; PRT; 530 AA.
AC Q90518;
RT

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DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Sodium channel alpha subunit (fragment).
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphae; Acanthopterygii; Percomorphae; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Nakazawa A.;
RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; D37976; BAA07194.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF00520; Ion_trans_1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON TER 530
SQ SEQUENCE 530 AA; 60164 MW; 2F9AB902C8F74071 CRC64;

Query Match      57.1%; Score 16; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMFVAVIFGSGYFL 16
DB 392 YMFVAVIFGSGYFL 407

RESULT 22
Q90378 PRELIMINARY; PRT; 711 AA.
ID Q90378
AC Q90378;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to sodium channel, voltage-gated, type 1, alpha
DE polypeptide.
GN Name=zgc:55600;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.O., Ussin T.B., Toshynki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Mair M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=whole body;
RA Strausberg R.;
DR Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044197; AAH44197.1; -.
DR HSSP; P08104; I0G9.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW SEQUENCE 711 AA; 80547 MW; 0BDE497E3BF85033 CRC64;

Query Match 57.1%; Score 16; DB 2; Length 711;
Best Local Similarity 100.0%; Pred. No. 7, 7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YMFVYVIFLGSFYL 16
Db 382 YMFVYVIFLGSFYL 397

RESULT 23
ID Q28371 PRELIMINARY; PRT; 1834 AA.
AC Q28371;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Skeletal muscle sodium channel alpha-subunit.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_Taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle plasma membrane;
RA Stephan D.J., Wang J., Spier S., Hoffman E.P.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; U25990; AAA67366.1; -.
DR HSSP; P04775; 1BYV.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0005248; P:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR008052; Na_channel4.
DR InterPro; IPR010526; Na_trans_assoc.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF06512; IQ_1.
DR Pfam; PF06512; Na_trans_assoc_1.
DR PRINTS; PR00170; NACHANNEL.
DR PRINTS; PR01665; NACHANNEL4.
DR SMART; SM00015; IQ_1.
DR PROSITE; PS50096; IQ_1.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.

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SQ SEQUENCE 1834 AA; 207485 MW; 01D62B25CD577D97 CRC64;

Query Match 57.1%; Score 16; DB 2; Length 1834;
Best Local Similarity 100.0%; Pred. No. 1, 6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 IFLGSFYINLILAVV 24
Db 425 IFLGSFYINLILAVV 440

RESULT 24
ID CIN3 RAT STANDARD; PRT; 1951 AA.
AC P08104;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sodium channel protein type III alpha subunit (Voltage-gated sodium
DE channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha
DE subunit) (Voltage-gated sodium channel subtype III).
GN Name=Scn3a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Miscar;
RX MEDLINE=88137594; PubMed=2449363;
RA Kayano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
RT Primary structure of rat brain sodium channel III deduced from the
RT cDNA sequence.
RL FEBS Lett. 228:187-194(1988).
CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC of excitable membranes. Assuming opened or closed conformations in
CC response to the voltage difference across the membrane, the
CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC 3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC hydrophobic segments (S1-S2, S3-S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL; Y00766; CAA68735.1; -.
DR PIR; S00320; S00320.
DR PDB; 1OG9; NMR; A=156-176.
DR RGD; 3635; Scn3a.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF06512; IQ_1.
DR PRINTS; PR00170; NACHANNEL.

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DR PROSITE, PS50096; IQ; FALSE NEG.
KW 3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Repeat; Sodium channel; Transmembrane;
KW Voltage-gated channel.
FT REPEAT 110 455
FT REPEAT 693 965
FT REPEAT 1139 1450
FT REPEAT 1459 1757
FT TRANSMEM 124 147
FT TRANSMEM 156 175
FT TRANSMEM 189 207
FT TRANSMEM 214 233
FT TRANSMEM 249 273
FT TRANSMEM 401 426
FT TRANSMEM 706 730
FT TRANSMEM 742 765
FT TRANSMEM 774 793
FT TRANSMEM 800 820
FT TRANSMEM 836 856
FT TRANSMEM 910 935
FT TRANSMEM 1153 1176
FT TRANSMEM 1190 1215
FT TRANSMEM 1222 1243
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FT TRANSMEM 1289 1310
FT TRANSMEM 1393 1419
FT TRANSMEM 1473 1496
FT TRANSMEM 1508 1531
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FT CARBOHYD 1085 1085
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FT CARBOHYD 1331 1331
SQ SEQUENCE 1951 AA; 221385 MM; 74B5B51524BD10E CRC64;

Query Match 57.1%; Score 16; DB 1; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMIFVYVIFGSPYL 16
DB 400 YMIFVYVIFGSPYL 415

RESULT 25
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AC Q9C007;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Voltage-gated sodium channel alpha subunit splice variant SCN3A-
DE s.
GN Name=SCN3A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeong S.-Y., Goto J., Kanazawa I.,

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RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AF225986; AAK00218.1; -.
DR HSSP; P04775; 1BYJ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrypL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR01696; Na_channel.
DR Pfam; PF00520; Na_trans_assoc.
DR Pfam; PF00612; Ion_trans_4.
DR Pfam; PF06512; Na_trans_assoc_1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ_1.
DR PROSITE; PS50096; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1951 AA; 221517 MM; 99AD4C032CE124AB CRC64;

Query Match 57.1%; Score 16; DB 2; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMIFVYVIFGSPYL 16
DB 400 YMIFVYVIFGSPYL 415

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Search completed: January 27, 2005, 17:51:30
Job time : 96.5 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 27, 2005, 17:36:50 ; Search time 22.5 Seconds
(without alignments)
82.529 Million cell updates/sec

Title: US-10-608-584-1

Perfect score: 28

Sequence: 1 YMIFFVLIVIGSFYILNLIIVAVMAY 28

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size: 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 100 summaries

Database:

Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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7	21	75.0	1977	4	US-09-919-039-367
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9	21	75.0	1984	4	US-09-457-571-10
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14	21	75.0	1989	4	US-10-162-012-24
15	20	71.4	1836	4	US-09-562-737-81
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17	16	57.1	1956	4	US-08-843-325-10
18	16	57.1	1956	4	US-09-527-013-10
19	13	46.4	1956	4	US-08-843-325-12
20	13	46.4	1956	4	US-09-527-013-2
21	13	46.4	1957	4	US-08-669-656A-2
22	13	46.4	1957	4	US-08-669-656A-8
23	13	46.4	2132	4	US-08-669-656A-6
24	12	42.9	1024	4	US-09-562-737-83
25	12	42.9	1233	4	US-09-354-147C-7
26	12	42.9	1243	4	US-09-354-147C-8
27	12	42.9	1791	4	US-09-354-147C-42

28	11	39.3	1976	3	US-09-024-020B-9	Sequence 9, Appl
29	11	39.3	1976	3	US-09-425-043-9	Sequence 9, Appl
30	11	39.3	1978	3	US-09-024-020B-3	Sequence 3, Appl
31	11	39.3	1978	3	US-09-425-043-3	Sequence 3, Appl
32	11	39.3	1988	3	US-09-024-020B-4	Sequence 4, Appl
33	11	39.3	1988	3	US-09-425-043-4	Sequence 4, Appl
34	11	39.3	2016	4	US-09-634-920-4	Sequence 4, Appl
35	11	39.3	2016	4	US-09-514-907A-2	Sequence 2, Appl
36	11	39.3	2016	4	US-09-896-994-2	Sequence 2, Appl
37	11	39.3	2016	4	US-09-840-125-4	Sequence 4, Appl
38	11	39.3	2016	4	US-09-562-737-82	Sequence 8, Appl
39	9	32.1	1024	4	US-09-562-737-84	Sequence 8, Appl
40	9	32.1	1024	4	US-09-562-737-85	Sequence 8, Appl
41	9	32.1	1024	4	US-09-562-737-86	Sequence 8, Appl
42	9	32.1	1024	4	US-09-562-737-87	Sequence 8, Appl
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44	9	32.1	1024	4	US-09-562-737-89	Sequence 8, Appl
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46	9	32.1	1765	4	US-09-354-147C-2	Sequence 2, Appl
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49	8	28.6	1820	3	US-07-998-289B-8	Sequence 8, Appl
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58	6	21.4	42	5	PCT-US93-08528-111	Sequence 311, Ap
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62	6	21.4	44	5	PCT-US93-08528-112	Sequence 312, Ap
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78	6	21.4	133	4	US-09-270-767-38939	Sequence 38939, A
79	6	21.4	133	4	US-09-270-767-54156	Sequence 54156, A
80	6	21.4	136	4	US-09-248-796A-22644	Sequence 22644, A
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82	6	21.4	147	4	US-09-270-767-53313	Sequence 53313, A
83	6	21.4	150	4	US-09-328-352-7806	Sequence 7806, Ap
84	6	21.4	159	3	US-08-796-792-2	Sequence 2, Appl
85	6	21.4	159	4	US-09-491-795-2	Sequence 2, Appl
86	6	21.4	184	4	US-09-134-000C-6724	Sequence 6724, Ap
87	6	21.4	194	4	US-09-489-039A-8286	Sequence 8286, Ap
88	6	21.4	200	3	US-09-134-001C-1099	Sequence 3099, Ap
89	6	21.4	208	1	US-07-935-309-2	Sequence 2, Appl
90	6	21.4	208	2	US-08-039-364-2	Sequence 2, Appl
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92	6	21.4	208	3	US-08-718-904-7	Sequence 7, Appl
93	6	21.4	208	3	US-09-181-974-2	Sequence 2, Appl
94	6	21.4	208	3	US-09-158-710-2	Sequence 2, Appl
95	6	21.4	208	3	US-09-518-950-2	Sequence 2, Appl
96	6	21.4	208	4	US-09-449-249-5	Sequence 5, Appl
97	6	21.4	208	4	US-09-449-249-7	Sequence 7, Appl
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100	6	21.4	261	4	US-09-522-714-6	Sequence 6, Appl

ALIGNMENTS

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RESULT 1
US-08-836-325-7
; Sequence 7, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 02-NOV-1995
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2005 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-325-7

Query Match      100.0%; Score 28; DB 3; Length 2005;
Best Local Similarity 100.0%; Pred. No. 2.3e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 YWIFVLVIFLGSFYLNILILAVVMAY 28
Db      401 YWIFVLVIFLGSFYLNILILAVVMAY 428
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RESULT 2
US-09-457-571-7
; Sequence 7, Application US/09457571
; Patent No. 6703486
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; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-DEC-1999
; APPLICATION NUMBER: US/09/457,571
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,325
; FILING DATE: 02-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2005 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-457-571-7

Query Match      100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 2.3e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY      1 YWIFVLVIFLGSFYLNILILAVVMAY 28
Db      401 YWIFVLVIFLGSFYLNILILAVVMAY 428
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RESULT 3
US-08-836-325-15
; Sequence 15, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
```

TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Theorec
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-836-325-15
Query Match 75.0%; Score 21; DB 3; Length 1835;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 VIFLSFYINILAVVMAY 28
Db 363 VIFLSFYINILAVVMAY 383
RESULT 4
US-09-457-571-15
Sequence 15, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-457-571-15
Query Match 75.0%; Score 21; DB 4; Length 1835;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 VIFLSFYINILAVVMAY 28
Db 363 VIFLSFYINILAVVMAY 383
RESULT 5
US-08-836-325-16
Sequence 16, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-16

Query Match
Best Local Similarity 75.0%; Score 21; DB 3; Length 1969;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VFILGSFYILNLIILAVVAMAY 28
DB 385 VFILGSFYILNLIILAVVAMAY 405

RESULT 6
US-09-457-571-16
Sequence 16, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halsegoda, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-457-571-16

Query Match
Best Local Similarity 75.0%; Score 21; DB 4; Length 1969;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VFILGSFYILNLIILAVVAMAY 28
DB 385 VFILGSFYILNLIILAVVAMAY 405

RESULT 7
US-09-976-594-757
Sequence 757, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 757
LENGTH: 1977
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1719478CD1
US-09-976-594-757

Query Match
Best Local Similarity 75.0%; Score 21; DB 4; Length 1977;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VFILGSFYILNLIILAVVAMAY 28
DB 385 VFILGSFYILNLIILAVVAMAY 405

RESULT 8
US-09-919-039-367
Sequence 367, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 367
LENGTH: 1977
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6727066 1719478CD1
US-09-919-039-367

Query Match 75.0%; Score 21; DB 4; Length 1977;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VIFLGSFYILNLIILAVVAMAY 28
Db 385 VIFLGSFYILNLIILAVVAMAY 405

RESULT 9
US-08-836-325-10
Sequence 10, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-836-325-10

Query Match 75.0%; Score 21; DB 3; Length 1984;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VIFLGSFYILNLIILAVVAMAY 28
Db 385 VIFLGSFYILNLIILAVVAMAY 405

RESULT 10
US-09-457-571-10
Sequence 10, Application US/09457571
Patent No. 6703465
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-457-571-10

Query Match 75.0%; Score 21; DB 4; Length 1984;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VIFLGSFYILNLIILAVVAMAY 28

Db 385 VIFLGSFYILNIIILAVVAMAY 405

RESULT 11

US-08-836-325-11

Sequence 11, Application US/08836325

Patent No. 6110672

GENERAL INFORMATION:

APPLICANT: Mandel, Gail

APPLICANT: Halegoua, Simon

APPLICANT: Borden, Laurence A.

TITLE OF INVENTION: Peripheral Nervous System Specific

TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,

TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational

TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C

STREET: 1100 New York Ave., N. W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,325

FILING DATE: 2-MAY-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/14251

FILING DATE: 02-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/482,401

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/334,029

FILING DATE: 02-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0917.0240002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 1989 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

US-08-836-325-11

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

APPLICANT: Mandel, Gail

APPLICANT: Halegoua, Simon

APPLICANT: Borden, Laurence A.

TITLE OF INVENTION: Peripheral Nervous System Specific

TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,

TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational

TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using

TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C

STREET: 1100 New York Ave., N. W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/836,325

FILING DATE: 2-MAY-1997

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/14251

FILING DATE: 02-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/482,401

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/334,029

FILING DATE: 02-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0917.0240002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 1989 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: protein

US-08-836-325-12

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 VIFLGSFYILNIIILAVVAMAY 405

Query Match

Best Local Similarity 75.0%; Score 21; DB 3; Length 1989;

Matches 21; Conservative 0; Mismatches 0; Indels 0; G

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-457-571-11

Query Match 75.0%; Score 21; DB 4; Length 1989;
Best Local Similarity 100.0%; Pred.No.1.7e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VIFLGSFYILNLIILAVANAY 28
DB 385 VIFLGSFYILNLIILAVANAY 405

RESULT 14
US-09-457-571-12
Sequence 12, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-457-571-12

Query Match 75.0%; Score 21; DB 4; Length 1989;
Best Local Similarity 100.0%; Pred.No.1.7e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VIFLGSFYILNLIILAVANAY 28
DB 385 VIFLGSFYILNLIILAVANAY 405

RESULT 15
US-10-162-012-24
Sequence 24, Application US/10162012
Patent No. 6682597
GENERAL INFORMATION:
APPLICANT: Curtiss, Roy A.J.
APPLICANT: Siles-Santiago, Immaculada
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
FILE REFERENCE: 10448-190001
CURRENT APPLICATION NUMBER: US/10/162,012
CURRENT FILING DATE: 2002-06-04
PRIORITY APPLICATION NUMBER: US 60/209,845
PRIORITY FILING DATE: 2000-06-06
PRIORITY APPLICATION NUMBER: US 09/875,321
PRIORITY FILING DATE: 2001-06-06
PRIORITY APPLICATION NUMBER: PCT/US01/18340
PRIORITY FILING DATE: 2001-06-06
PRIORITY APPLICATION NUMBER: US 60/209,257
PRIORITY FILING DATE: 2000-06-05
PRIORITY APPLICATION NUMBER: US 09/875,423
PRIORITY FILING DATE: 2001-06-05
PRIORITY APPLICATION NUMBER: PCT/US01/18398
PRIORITY FILING DATE: 2001-06-05
PRIORITY APPLICATION NUMBER: US 60/209,238
PRIORITY FILING DATE: 2000-06-05
PRIORITY APPLICATION NUMBER: US 09/875,363
PRIORITY FILING DATE: 2001-06-05

PRIOR APPLICATION NUMBER: PCT/US01/16247
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/928,530
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: PCT/US01/25475
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/934,421
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/US01/26096
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/279,281
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 10/109,029
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: PCT/US02/09728
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US (not assigned)
PRIOR FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 1836
TYPE: PRT
ORGANISM: Homo sapiens
US-10-162-012-24

Query Match 71.4%; Score 20; DB 4; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFLGSFYLNLILAVVMAY 28
DB 431 IFLGSFYLNLILAVVMAY 450

RESULT 16
US-09-562-737-81
Sequence 81, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Hertz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 1024
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-81

Query Match 57.1%; Score 16; DB 4; Length 1024;
Best Local Similarity 100.0%; Pred. No. 7.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMIFVLVIFLGSFYL 16
DB 400 YMIFVLVIFLGSFYL 415

RESULT 17

US-08-843-417-10
Sequence 10, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHEetical: NO
ANTI-SENSE: NO
US-08-843-417-10

Query Match 57.1%; Score 16; DB 3; Length 1956;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMIFVLVIFLGSFYL 16
DB 373 YMIFVLVIFLGSFYL 388

RESULT 18
US-09-527-013-10
Sequence 10, Application US/09527013
Patent No. 6479259
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McAuliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA

COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527,013
FILING DATE: 16-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/843,417
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
MOLECULE TYPE: peptide
TOPOLOGY: unknown
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-527-013-10

Query Match 57.1%; Score 16; DB 4; Length 1956;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YMFVIVFLGSEYFL 16
DB 373 YMFVIVFLGSEYFL 388

RESULT 19
US-08-843-417-2
Sequence 2, Application US/08843417
Patent No. 6184349
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,417
FILING DATE: April 15, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William

REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: dorsal root ganglia
CELL TYPE: peripheral nerve
US-08-843-417-2

Query Match 46.4%; Score 13; DB 3; Length 1956;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FFVLVIFLGSEYFL 16
DB 375 FFVLVIFLGSEYFL 387

RESULT 20
US-09-527-013-2
Sequence 2, Application US/09527013
Patent No. 6479259
GENERAL INFORMATION:
APPLICANT: Herman, Ronald C
APPLICANT: Delgado, Stephen G
APPLICANT: Fish, Linda M
APPLICANT: Sangameswaran, Lakshmi
APPLICANT: Rabert, Douglas K
TITLE OF INVENTION: CLONED PERIPHERAL NERVE
TITLE OF INVENTION: TETRODOTOXIN-RESISTANT SODIUM CHANNEL alpha-SUBUNIT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 525 University Ave
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.A.
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527,013
FILING DATE: 16-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/843,417
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Schmonsees, William
REGISTRATION NUMBER: 31,796
REFERENCE/DOCKET NUMBER: 28340-P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)-324-7041
TELEFAX: (415)-324-0638
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1956 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: not relevant

MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: rat
 TISSUE TYPE: dorsal root ganglia
 CELL TYPE: peripheral nerve
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-527-013-2

Query Match 46.4%; Score 13; DB 4; Length 1956;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FFVLVIFLGSFYL 16
 DB 375 FFVLVIFLGSFYL 387

RESULT 21
 US-08-669-656A-2
 Sequence 2, Application US/08669656A
 Patent No. 6451554
 GENERAL INFORMATION:
 APPLICANT: Wood, John N.
 APPLICANT: Akopian, Armen N.
 TITLE OF INVENTION: Ion Channel
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZENECA Pharmaceuticals
 STREET: 1800 Concord Pike, P.O. Box 15437
 CITY: Wilmington
 STATE: Delaware
 COUNTRY: USA
 ZIP: 19850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/669,656A
 FILING DATE: 24-JUN-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Hohenschutz, Liza D.
 REGISTRATION NUMBER: 33,712
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 886-7466
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1957 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-669-656A-2

Query Match 46.4%; Score 13; DB 4; Length 1957;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FFVLVIFLGSFYL 16
 DB 375 FFVLVIFLGSFYL 387

RESULT 22
 US-08-669-656A-8
 Sequence 8, Application US/08669656A
 Patent No. 6451554
 GENERAL INFORMATION:
 APPLICANT: Wood, John N.
 APPLICANT: Akopian, Armen N.

TITLE OF INVENTION: Ion Channel
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZENECA Pharmaceuticals
 STREET: 1800 Concord Pike, P.O. Box 15437
 CITY: Wilmington
 STATE: Delaware
 COUNTRY: USA
 ZIP: 19850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/669,656A
 FILING DATE: 24-JUN-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Hohenschutz, Liza D.
 REGISTRATION NUMBER: 33,712
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 886-7466
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1957 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-669-656A-8

Query Match 46.4%; Score 13; DB 4; Length 1957;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FFVLVIFLGSFYL 16
 DB 375 FFVLVIFLGSFYL 387

RESULT 23
 US-08-669-656A-6
 Sequence 6, Application US/08669656A
 Patent No. 6451554
 GENERAL INFORMATION:
 APPLICANT: Wood, John N.
 APPLICANT: Akopian, Armen N.
 TITLE OF INVENTION: Ion Channel
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZENECA Pharmaceuticals
 STREET: 1800 Concord Pike, P.O. Box 15437
 CITY: Wilmington
 STATE: Delaware
 COUNTRY: USA
 ZIP: 19850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/669,656A
 FILING DATE: 24-JUN-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Hohenschutz, Liza D.
 REGISTRATION NUMBER: 33,712
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (302) 886-7466
 INFORMATION FOR SEQ ID NO: 6:

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-669-656A-6

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Query Match          46.4%; Score 13; DB 4; Length 2132;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 FVLVIFLGSFYL 16
Db      375 FVLVIFLGSFYL 387

```

```

RESULT 24
US-09-562-737-83
; Sequence 83, Application US/09562737
; Patent No. 6428967
; GENERAL INFORMATION:
; APPLICANT: Herz, Joachim
; APPLICANT: Goethardt, Michael
; TITLE OF INVENTION: LDL Receptor Signaling Pathways
; FILE REFERENCE: UTSW0708
; CURRENT APPLICATION NUMBER: US/09/562,737
; CURRENT FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 83
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-83

```

```

Query Match          42.9%; Score 12; DB 4; Length 1024;
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 FVLVIFLGSFYL 16
Db      404 FVLVIFLGSFYL 415

```

```

RESULT 25
US-09-354-147C-7
; Sequence 7, Application US/09354147C
; Patent No. 6573067
; GENERAL INFORMATION:
; APPLICANT: Dib-Hajj, Sulayman
; APPLICANT: Waxman, Stephen G.
; TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
; FILE REFERENCE: 44574-5004-01-US
; CURRENT APPLICATION NUMBER: US/09/354,147C
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 60/072,990
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: US 60/109,402
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: PCT/US99/02008
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (308)

```

```

; OTHER INFORMATION: Xaa is leu. Xaa results from a "y" in SEQ ID NO: 6.
US-09-354-147C-7

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Query Match          42.9%; Score 12; DB 4; Length 1233;
Best Local Similarity 100.0%; Pred. No. 0.00078;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      8 VIFLGSFYLINL 19
Db      184 VIFLGSFYLINL 195

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Search completed: January 27, 2005, 17:54:17
Job time : 23.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:32:04 ; Search time 86.5 Seconds
(without alignments)
116.120 Million cell updates/sec

Title: US-10-608-584-13
Perfect score: 28
Sequence: 1 CLTVFMVWVIGNLVNLFLALLLSF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_23Sep04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	1795	7	ADB78596 Human sod
2	28	100.0	1855	7	ADB78597 Human sod
3	28	100.0	1981	7	ABR83185 Human SCN
4	28	100.0	1998	7	ABR83184 Human SCN
5	28	100.0	1999	5	ABBO6026 Human adu
6	28	100.0	2005	4	AAB99676 Human adu
7	28	100.0	2005	4	AAB99677 Human neo
8	28	100.0	2005	5	ABBR83627 Human GEF
9	28	100.0	2005	7	ADB78604 Human sod
10	28	100.0	2005	7	ADB78603 Human sod
11	28	100.0	2005	7	ADB78605 Human sod
12	28	100.0	2005	7	ADCA6947 Human SCN
13	28	100.0	2009	4	AAB99674 Human adu
14	28	100.0	2009	5	ABG69292 Human sod
15	28	100.0	2009	5	ABG69291 Human sod
16	28	100.0	2009	5	ABG69293 Human sod
17	28	100.0	2009	5	ABG69289 Human sod
18	28	100.0	2009	5	ABG69290 Human sod
19	28	100.0	2009	5	ABBR83626 Human GEF
20	28	100.0	2009	5	AAE16776 Human tra
21	28	100.0	2009	7	ADB78599 Human sod
22	28	100.0	2009	7	ADB78595 Human sod
23	28	100.0	2009	7	ADB78593 Human sod
24	28	100.0	2009	7	ADB78594 Human sod
25	28	100.0	2009	7	ADB78598 Human sod

26	28	100.0	2009	7	ABR83180 Human SCN
27	28	100.0	2009	7	ADE57563 Human Pro
28	28	89.3	1976	7	ADE57386 Rat Prote
29	25	89.3	1978	2	AAW69361 Tetrodoto
30	25	89.3	1980	3	AAW69363 Tetrodoto
31	25	89.3	1980	5	AAO14927 Human sod
32	25	89.3	1980	7	ADB78600 Human sod
33	25	89.3	1980	7	ADB78606 Human sod
34	25	89.3	1988	2	AAW69362 Tetrodoto
35	24	85.7	1381	5	AAE20513 Human ion
36	24	85.7	1382	5	AAE20514 Human ion
37	24	85.7	1392	5	AAE20518 Human ion
38	24	85.7	1398	5	AAE20519 Human ion
39	24	85.7	1442	5	AAE20512 Human ion
40	24	85.7	1453	5	AAE20517 Human ion
41	24	85.7	1962	5	AAE20511 Human ion
42	24	85.7	1973	5	AAE20516 Human ion
43	24	85.7	1998	5	AAE20510 Human ion
44	24	85.7	2009	5	AAE20515 Human ion
45	24	82.1	1835	2	AAE92316 Periphra
46	23	82.1	1977	8	AAE99641 Periphra
47	23	82.1	1977	8	ADE77202 Human pro
48	23	82.1	1977	8	ADL13028 Human ate
49	23	82.1	1978	7	ADE54553 Human Pro
50	23	82.1	1978	7	ADE54549 Human Pro
51	23	82.1	1984	2	AAE99639 Periphra
52	23	82.1	1984	7	ADE54547 Rat Prote
53	23	82.1	1984	7	ADE54551 Rat Prote
54	23	82.1	1984	7	ADE63027 Rat Prote
55	23	82.1	1989	2	AAE92317 Periphra
56	23	82.1	1989	2	AAE99640 Periphra
57	22	78.6	1836	7	ADE57388 Human Pro
58	22	78.6	1836	7	ADE59630 Human Pro
59	22	78.6	1836	7	ADE63029 Human Pro
60	22	78.6	1836	8	ADQ17412 Human sof
61	21	75.0	1024	5	ABBO4858 LDL recep
62	21	75.0	1107	6	ABR41495 Human DIT
63	21	75.0	1366	7	ADJ68488 Human hea
64	21	75.0	1366	8	ADL06575 Human tum
65	21	75.0	1950	4	ADB78607 Human adu
66	21	75.0	1951	4	AAE99678 Human adu
67	21	75.0	1951	4	AAE99679 Human neo
68	21	75.0	1951	4	ADE59628 Rat Prote
69	21	75.0	1951	8	ADL06576 Human tum
70	21	75.0	2000	5	ABBO6027 Human sod
71	21	75.0	2000	8	ADK81762 Human Nav
72	21	75.0	2015	4	AAE82242 Human SCN
73	21	75.0	2015	7	ADP56441 Human Nav
74	21	75.0	2015	8	ADM34001 Human SCN
75	21	75.0	2015	8	ADM33999 Human SCN
76	21	75.0	2016	4	AAW23994 Human hml
77	21	75.0	2016	4	AAE82239 Human SCN
78	21	75.0	2016	4	AAE82240 Human SCN
79	21	75.0	2016	4	AAE82245 Human SCN
80	21	75.0	2016	4	AAE82243 Human SCN
81	21	75.0	2016	4	AAE82244 Human SCN
82	21	75.0	2016	4	AAE82241 Human SCN
83	21	75.0	2016	7	ADD44756 Human Pro
84	21	75.0	2016	7	ADE55106 Human Pro
85	21	75.0	2016	8	ADM33997 Human SCN
86	21	75.0	2016	8	ADM33995 Human SCN
87	21	75.0	2019	2	AAE67913 Cardiac s
88	17	60.7	2100	2	AAW89579 Cardiac p
89	17	60.7	2105	2	AAW57772 Mueca dom
90	17	60.7	2105	2	AAW89577 Calcium P
91	17	60.7	2131	4	ABW64743 Drosophi1
92	17	60.7	2131	8	ADL30141 Drosophi1
93	17	60.7	2131	8	ADL30146 Drosophi1
94	16	57.1	1011	2	AAE99638 Periphra
95	16	57.1	1011	2	AAE99638 Periphra
96	13	46.4	115	5	ABG37774 Human pep
97	12	42.9	2104	2	AAW57773 Mueca dom
98	12	42.9	2104	2	AAW89578 Calcium p

99 10 35.7 125 8 ABO54760
100 10 35.7 2020 2 AAR06584

Ab054760 Human gen
Aar06584 Cardiac s

ALIGNMENTS

RESULT 1
ADB78596

ID ADB78596 standard; protein; 1795 AA.

XX ADB78596;

DT 04-DEC-2003 (first entry)

DE Human sodium channel subunit mutant SEQ ID NO:140.

KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrctic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;
KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.

OS Synthetic.
XX Homo sapiens.

PN WO2003008574-A1.

PD 30-JAN-2003.

PF 08-JUL-2002; 2002MO-AU000910.

PR 18-JUL-2001; 2001AU-00006452.

PR 05-MAR-2002; 2002AU-00000910.

PR 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

PA (WALL/) WALLACE R W.

PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;

DR N-PSDB; ADB78635.

PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.

PS Claim 13; SEQ ID NO 140; 106bp; English.

CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyrctic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemia, periodic paralysis, myotonia, malignant hyperthermia, Alz-
CC hementia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperplexia, anxiety,
CC depression, phobias, obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Barter's syndrome, polycystic kidney disease,
CC Dent's disease, hypernatraemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour

CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp://wipo.int/pub/published_pat_sequences.
XX

SO Sequence 1795 AA;

Query Match 100.0%; Score 28; DB 7; Length 1795;
Best Local Similarity 100.0%; Pred. NO. 6.7e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTVMVMVYIGNLVINLFLALLSSP 28
Db 968 CLTVMVMVYIGNLVINLFLALLSSP 995

RESULT 2
ADB78597

ID ADB78597 standard; protein; 1855 AA.

XX ADB78597;

DT 04-DEC-2003 (first entry)

DE Human sodium channel subunit mutant SEQ ID NO:141.

KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyrctic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;
KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.

OS Synthetic.

XX Homo sapiens.

PN WO2003008574-A1.

PD 30-JAN-2003.

PF 08-JUL-2002; 2002MO-AU000910.

PR 18-JUL-2001; 2001AU-00006452.

PR 05-MAR-2002; 2002AU-00000910.

PR 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

PA (WALL/) WALLACE R W.
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;

DR N-PSDB; ADB78636.

PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.

PS Claim 13; SEQ ID NO 141; 106bp; English.

CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyrctic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquilizer, analgesic, neuroprotective, inotropic, antipyrctic,
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human

CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

CC Sequence 1855 AA;

Query Match 100.0%; Score 28; DB 7; Length 1855;
 Best Local Similarity 100.0%; Pred. No. 6.9e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CLTVFMVMVYIGNLVNLFPLALLSSP 28
 Db 968 CLTVFMVMVYIGNLVNLFPLALLSSP 995

RESULT 3

ABR83185 ID ABR83185 standard; protein; 1981 AA.

AC ABR83185;

DT 15-JAN-2004 (first entry)

XX Human SCN1A splice variant -84P:SCN1ADELP654-681.

XX SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
 KW neuroprotective; anesthetic; cytosolic; cerebroprotective; cardiac;
 KM hypotensive; gene therapy; human; splice variant.

XX Homo sapiens.

XX WO2003072751-A2.

XX 04-SEP-2003.

XX 25-FEB-2003; 2003WO-US006010.

XX 25-FEB-2002; 2002US-0359382P.

XX (UYVA-) UNIV VANDERBILT.

XX George AL, Loebsin C;

XX WPI; 2003-712725/67.

XX N-PSDB; ACF57880.

XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in
 PT screening for modulators, for treating e.g. epilepsy.

XX Disclosure; Page 162-169; 176pp; English.

XX The invention relates to a recombinantly expressed and isolated human
 CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
 CC incorporated into a cell, is used to screen for specific modulators,
 CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
 CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
 CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
 CC motor endplate diseases, hypertension, congestive heart failure and
 CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
 CC and metastatic cancer cell lines). These activities can also be provided
 CC by gene therapy vectors that express (I) or the modulators. The
 CC modulators, also antibodies directed against (I), are used to detect
 CC sodium channel polypeptides. The present sequence represents a human

CC SCN1A splice variant 84P:SCN1ADELP654-681
 XX Sequence 1981 AA;

Query Match 100.0%; Score 28; DB 7; Length 1981;
 Best Local Similarity 100.0%; Pred. No. 7.3e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CLTVFMVMVYIGNLVNLFPLALLSSP 28
 Db 940 CLTVFMVMVYIGNLVNLFPLALLSSP 967

RESULT 4

ABR83184 ID ABR83184 standard; protein; 1998 AA.

AC ABR83184;

DT 15-JAN-2004 (first entry)

XX Human SCN1A splice variant -33P:SCN1ADELP671-681.

XX SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
 KW neuroprotective; anesthetic; cytosolic; cerebroprotective; cardiac;
 KM hypotensive; gene therapy; human; splice variant.

XX Homo sapiens.

XX WO2003072751-A2.

XX 04-SEP-2003.

XX 25-FEB-2003; 2003WO-US006010.

XX 25-FEB-2002; 2002US-0359382P.

XX (UYVA-) UNIV VANDERBILT.

XX George AL, Loebsin C;

XX WPI; 2003-712725/67.

XX N-PSDB; ACF57879.

XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in
 PT screening for modulators, for treating e.g. epilepsy.

XX Disclosure; Page 148-156; 176pp; English.

XX The invention relates to a recombinantly expressed and isolated human
 CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
 CC incorporated into a cell, is used to screen for specific modulators,
 CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
 CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
 CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
 CC motor endplate diseases, hypertension, congestive heart failure and
 CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
 CC and metastatic cancer cell lines). These activities can also be provided
 CC by gene therapy vectors that express (I) or the modulators. The
 CC modulators, also antibodies directed against (I), are used to detect
 CC sodium channel polypeptides. The present sequence represents a human
 CC SCN1A splice variant 33P:SCN1ADELP671-681 encoding cDNA

XX Sequence 1998 AA;

Query Match 100.0%; Score 28; DB 7; Length 1998;
 Best Local Similarity 100.0%; Pred. No. 7.4e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CLTVFMVMVYIGNLVNLFPLALLSSP 28
 Db 957 CLTVFMVMVYIGNLVNLFPLALLSSP 984

RESULT 5
 ABB06026
 ID ABB06026 standard; protein; 1999 AA.
 XX
 AC ABB06026;
 XX
 DT 10-MAY-2002 (first entry)
 XX
 DE Human sodium channel SCN1A protein SEQ ID NO:2.
 XX
 KW Human; sodium channel; SCN1A; chromosome 2q24;
 KM familial hypercalcaemic periodic paralysis; motor endplate disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200196552-A1.
 XX
 PD 20-DEC-2001.
 XX
 PF 12-JUN-2001; 2001WO-JP004956.
 XX
 PR 13-JUN-2000; 2000JP-00177540.
 PR 13-JUN-2000; 2000JP-00177544.
 XX
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 XX
 PI Kanazawa I, Goto J, Jeong S;
 XX
 DR MPI; 2002-098066/13.
 XX
 DR N-PSDB; ABL39689.
 XX
 PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
 PT studying physiological mechanism in which excitant cells participate and
 XX causes of diseases and developing drugs for motor endplate disease.
 XX
 PS Claim 1; Page 40-49; 88pp; Japanese.
 XX
 CC The present invention describes human sodium channels SCN1A and SCN3A.
 CC The present sequence represents the human sodium channel SCN1A. SCN1A and
 CC SCN3A have been located to the human chromosome 2 long arm, positions
 CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
 CC studying the physiological mechanism in which excitant cells participate
 CC and cause human diseases, and in developing remedies for e.g. familial
 CC hypercalcaemic periodic paralysis of extremities and motor endplate
 CC disease
 CC
 XX
 SQ Sequence 1999 AA;
 XX
 Query Match 100.0%; Score 28; DB 5; Length 1999;
 Best Local Similarity 100.0%; Pred. No. 7.4e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTVMVMVIGNVLVNLFLALLLSF 28
 DB 958 CTTVMVMVIGNVLVNLFLALLLSF 985
 XX
 RESULT 6
 AAB99676
 ID AAB99676 standard; protein; 2005 AA.
 XX
 AC AAB99676;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human adult form of SCN2A protein sequence SEQ ID NO:35.
 XX
 KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
 KM diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
 KW anticonvulsant; neuroprotective.
 XX
 OS Homo sapiens.

XX
 PN WO200138564-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 24-NOV-2000; 2000WO-CA001404.
 XX
 PR 26-NOV-1999; 99US-0167623P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Rouleau GA, Lafreniere RG, Rochefort D, Coesette P, Ragsdale D;
 XX
 DR MPI; 2001-355945/37.
 XX
 DR N-PSDB; AAH55793.
 XX
 PT Determining a predisposition to epilepsy and/or development of epilepsy
 PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
 XX variant, equivalent, or mutation which shows a linkage disequilibrium.
 XX
 PS Disclosure; Page 123-130; 268pp; English.
 XX
 CC The present invention describes a method (M1) of determining an
 CC individual's predisposition to epilepsy and/or development of epilepsy,
 CC as well as predicting the individual's response to medication. The method
 CC comprises determining the genotype of at least one gene selected from
 CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent or mutation which
 CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
 CC channel genes located on chromosome 2. The idiopathic generalised
 CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
 CC q31. Compounds identified as modulators of the biological activity of
 CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
 CC or other neurological disorders. They have anticonvulsant and
 CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
 CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
 CC invention
 CC
 XX
 SQ Sequence 2005 AA;
 XX
 Query Match 100.0%; Score 28; DB 4; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 7.4e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTVMVMVIGNVLVNLFLALLLSF 28
 DB 959 CTTVMVMVIGNVLVNLFLALLLSF 986
 XX
 RESULT 7
 AAB99677
 ID AAB99677 standard; protein; 2005 AA.
 XX
 AC AAB99677;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human neonatal form of SCN2A protein sequence SEQ ID NO:36.
 XX
 KW Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
 KM diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
 KW anticonvulsant; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 PN WO200138564-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 24-NOV-2000; 2000WO-CA001404.
 XX
 PR 26-NOV-1999; 99US-0167623P.
 XX

PA (UWMC-) UNIV MCGILL.
 XX Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
 XX WPI; 2001-355945/37.
 DR N-PSDB; AAH55794.
 XX
 PT Determining a predisposition to epilepsy and/or development of epilepsy
 PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
 PT variant, equivalent, or mutation which shows a linkage disequilibrium.
 XX
 PS Disclosure; Page 131-138; 268pp; English.
 XX
 CC The present invention describes a method (M1) of determining an
 CC individual's predisposition to epilepsy and/or development of epilepsy,
 CC as well as predicting the individual's response to medication. The method
 CC comprises determining the genotype of at least one gene selected from
 CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
 CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
 CC channel genes located on chromosome 2. The idiopathic generalized
 CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
 CC q31. Compounds identified as modulators of the biological activity of
 CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
 CC or other neurological disorders. They have anticonvulsant and
 CC neuroprotective activities. AAH55763 to AAH56164 and AAH9674 to AAH9679
 CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
 CC oligonucleotides and proteins given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 2005 AA;
 XX
 QY Query Match 100.0%; Score 28; DB 4; Length 2005;
 Db Best Local Similarity 100.0%; Pred. No. 7,4e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTMMVWVIGNLVNLFLALLLSSP 28
 Db 959 CTTTMMVWVIGNLVNLFLALLLSSP 986
 XX
 RESULT 8
 ABB83627
 ID ABB83627 standard; protein; 2005 AA.
 XX
 AC ABB83627;
 XX
 DT 10-OCT-2002 (first entry)
 XX
 DE Human GEFs+ protein with SCN2A mutation.
 XX
 KW Human; GEFs+; SCN2A; mutant; muten;
 KW generalized epilepsy with febrile seizure plus.
 XX
 OS Homo sapiens.
 XX
 PN JP2002136289-A.
 XX
 PD 14-MAY-2002.
 XX
 PF 01-NOV-2000; 2000JP-00334969.
 XX
 PR 01-NOV-2000; 2000JP-00334969.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA (RIKA) RIKAGAKU KENKYUSHO.
 XX
 DR WPI; 2002-552308/59.
 DR N-PSDB; ABQ79201.
 XX
 PT A human polynucleotide which is complementary to an mRNA transcribed from
 PT a generalized epilepsy with febrile seizure plus (GEFS+)-related gene
 PT useful for diagnosing GEFS+.
 XX

PS Claim 10; Page 29-34; 37pp; Japanese.
 XX
 CC This invention relates to a human polynucleotide which is complementary
 CC to an mRNA transcribed from a "generalized epilepsy with febrile seizure
 CC plus" (GEFS+)-related gene. The gene is useful for diagnosing GEFS+. The
 CC present sequence represents the human GEFs+ protein sequence with SCN2A
 CC mutation
 XX
 SQ Sequence 2005 AA;
 XX
 QY Query Match 100.0%; Score 28; DB 5; Length 2005;
 Db Best Local Similarity 100.0%; Pred. No. 7,4e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTMMVWVIGNLVNLFLALLLSSP 28
 Db 959 CTTTMMVWVIGNLVNLFLALLLSSP 986
 XX
 RESULT 9
 ADB78604
 ID ADB78604 standard; protein; 2005 AA.
 XX
 AC ADB78604;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human sodium channel subunit mutant SEQ ID NO:148.
 XX
 KW muten; mutant; ion channel; ion channel subunit; ICS; noctropic;
 KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antianginal;
 KW antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;
 KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO2003008574-A1.
 XX
 PD 30-JAN-2003.
 XX
 PF 08-JUL-2002; 2002WO-AU000910.
 XX
 PR 18-JUL-2001; 2001AU-00006452.
 PR 05-MAR-2002; 2002AU-00000910.
 PR 13-MAY-2002; 2002AU-00002292.
 XX
 PA (BION-) BIONOMICS LTD.
 PA (WALL) WALLACE R W.
 XX
 PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
 PI Berkovic SF, Scheffer IE;
 XX
 DR WPI; 2003-239332/23.
 DR N-PSDB; ADB78643.
 XX
 PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 148; 106pp; English.
 XX
 CC The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has noctropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antianginal, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquilizer, analgesic, nephrotoxic, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an

CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTFPMWVVGIVLVNLFLLILSSSF 28
|||
Db 959 CLTFPMWVVGIVLVNLFLLILSSSF 986

RESULT 10
ADB78603
ID ADB78603 standard; protein; 2005 AA.

AC ADB78603;

DT 04-DEC-2003 (first entry)

DE Human sodium channel subunit mutant SEQ ID NO:147.

KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquilliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.

OS Synthetic.

OS Homo sapiens.

PN WO2003008574-A1.

PD 30-JAN-2003.

PF 08-JUL-2002; 2002MO-AU000910.

PR 18-JUL-2001; 2001AU-00006452.

PR 05-MAR-2002; 2002AU-00000910.

PR 13-MAY-2002; 2002AU-00002292.

PA (BION-) BIONOMICS LTD.

PA (WALL-) WALLACE R W.

PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;

XX WPI; 2003-239332/23.

XX N-PSDB; ADB78642.

XX

XX

XX

XX

XX

CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neurolipic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
Best Local Similarity 100.0%; Pred. No. 7.4e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTFPMWVVGIVLVNLFLLILSSSF 28
|||
Db 959 CLTFPMWVVGIVLVNLFLLILSSSF 986

RESULT 11
ADB78605
ID ADB78605 standard; protein; 2005 AA.

AC ADB78605;

DT 04-DEC-2003 (first entry)

DE Human sodium channel subunit mutant SEQ ID NO:149.

KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KW antidepressant; antiparkinsonian; neuroleptic; tranquilliser; analgesic;
KW nephrotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.

OS Synthetic.

OS Homo sapiens.

PN WO2003008574-A1.

PD 30-JAN-2003.

PF 08-JUL-2002; 2002MO-AU000910.

PR 18-JUL-2001; 2001AU-00006452.

PR 05-MAR-2002; 2002AU-00000910.

PR 13-MAY-2002; 2002AU-00002292.

PA (BION-) BIONOMICS LTD.

PA (WALL-) WALLACE R W.

PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;

XX WPI; 2003-239332/23.

XX

DR N-PSDB; ADB78644.
 XX
 XX Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 149; 106pp; English.
 XX
 XX The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICs) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
 CC antihypertensive, antimigraine, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquilizer, analgesic, nephroprotective, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemia, periodic paralysis, myotonias, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinemic hypoglycemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at http://wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 2005 AA;
 XX
 XX Query Match 100.0%; Score 28; DB 7; Length 2005;
 XX Best Local Similarity 100.0%; Pred. No. 7,4e-18;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLTFFMMWVWVIGNLVNLFLALLSSP 28
 Db 959 CLTFFMMWVWVIGNLVNLFLALLSSP 986
 XX
 XX RESULT 12
 XX ADC46947
 XX ID ADC46947 standard; protein; 2005 AA.
 XX
 XX ADC46947;
 XX
 XX 18-DEC-2003 (first entry)
 XX
 XX Human SCN2A amino acid sequence #SEQ ID 3.
 DE
 XX SCN2A, voltage-gated ion channel, human, neuroprotective; gene therapy;
 KM vaccine; Alzheimer's disease.
 KM
 XX
 XX Homo sapiens.
 OS
 XX
 XX MO2003060525-A1.
 PN
 XX
 XX 24-JUL-2003.
 PD
 XX
 XX 16-JAN-2003; 2003MO-EP000400.
 PF
 XX
 XX 17-JAN-2002; 2002EP-00001236.
 PR
 XX 17-JAN-2002; 2002US-0348674P.
 PA (EVOTEC) EVOTEC NEUROSCIENCES GMBH.
 XX
 XX Hipfel R, Von Der Kammer H, Pohlner J;
 PI

XX
 DR WPI; 2003-598580/56.
 DR N-PSDB; ADC46947.
 XX
 XX Diagnosing or prognosticating a neurodegenerative disease by detecting
 PT the level or activity of transcription or translation products of the
 PT gene coding for the voltage-gated ion channel SCN2A.
 XX
 PS Disclosure; Fig 9; 67pp; English.
 XX
 XX The invention relates to a method for diagnosing or prognosticating a
 CC neurodegenerative disease in a subject, or determining whether a subject
 CC is at increased risk of developing the disease. The method comprises
 CC detecting the level and/or activity of a transcription or translation
 CC product of the gene coding for the voltage-gated ion channel SCN2A. The
 CC modulator of an activity and/or of a level of at least one substance is
 CC useful for preparing a composition for treating or preventing a
 CC neurodegenerative disease, in particular Alzheimer's disease. The current
 CC sequence represents the human SCN2A amino acid sequence.
 CC
 SQ Sequence 2005 AA;
 XX
 XX Query Match 100.0%; Score 28; DB 7; Length 2005;
 XX Best Local Similarity 100.0%; Pred. No. 7,4e-18;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLTFFMMWVWVIGNLVNLFLALLSSP 28
 Db 959 CLTFFMMWVWVIGNLVNLFLALLSSP 986
 XX
 XX RESULT 13
 XX AAB99674
 XX ID AAB99674 standard; protein; 2009 AA.
 XX
 XX AAB99674;
 XX
 XX 04-SEP-2001 (first entry)
 DT
 XX
 XX Human adult form of SCN1A protein sequence SEQ ID NO.3.
 DE
 XX Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
 KM diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
 KM anticonvulsant; neuroprotective.
 KM
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200138564-A2.
 PN
 XX
 XX 31-MAY-2001.
 PD
 XX
 XX 24-NOV-2000; 2000WO-CA001404.
 PF
 XX
 XX 26-NOV-1999; 99US-0167623P.
 PR
 XX (UMC-) UNIV MCGILL.
 PA
 XX Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
 XX
 XX WPI; 2001-355945/37.
 DR
 XX N-PSDB; AAH55763.
 DR
 XX
 XX Determining a predisposition to epilepsy and/or development of epilepsy
 PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
 PT variant, equivalent, or mutation which shows a linkage disequilibrium.
 XX
 PS Disclosure; Page 96-104; 268pp; English.
 XX
 XX The present invention describes a method (M1) of determining an
 CC individual's predisposition to epilepsy and/or development of epilepsy,
 CC as well as predicting the individual's response to medication. The method
 CC comprises determining the genotype of at least one gene selected from
 CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which

CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
 CC channel genes located on chromosome 2. The idiopathic generalised
 CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
 CC q31. Compounds identified as modulators of the biological activity of
 CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
 CC or other neurological disorders. They have anticonvulsant and
 CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
 CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
 CC oligonucleotides and proteins given in the exemplification of the present
 CC invention
 CC XX

Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 4; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 7.5e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTFFMMVWVIGNLVNLVNLFLALLSSSF 28
 Db 968 CLTFFMMVWVIGNLVNLVNLFLALLSSSF 995

RESULT 14

ABG69292 standard; protein; 2009 AA.

ABG69293;

21-OCT-2002 (first entry)

Human sodium channel alpha 1-subunit (SCN1A) variant protein #4.

Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
 generalised epilepsy with febrile seizures plus; myasthenia;
 sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
 inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
 schizophrenia; hyperkplexia; anticonvulsant; analgesic; neuroprotective;
 nootropic; anti-Parkinsonian; neuroleptic.

Homo sapiens.

WO200250096-A1.

27-JUN-2002.

20-DEC-2001; 2001WO-AU001648.

20-DEC-2000; 2000AU-00002203.

(BION-) BIONOMICS LTD.

Wallace RH, Mulley JC, Berkovic SF;

WPI; 2002-528445/56.

New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
 gated sodium channel, useful for diagnosis of epilepsy, particularly
 generalized epilepsy with febrile seizures plus.

Claim 53; Page 147-157; 198pp; English.

The invention relates to a nucleic acid molecule encoding a mutant alpha
 subunit of a mammalian voltage-gated sodium channel. The DNA and the
 polypeptide may be used in the diagnosis of epilepsy, in particular
 CC generalised epilepsy with febrile seizures plus, and other disorders
 CC associated with sodium channel dysfunction. The polypeptide is useful for
 CC the screening of candidate pharmaceutical agents, where high throughput
 CC screening techniques are employed. The sequences are also useful in the
 CC manufacture of a medicament for the treatment of a disorder associated
 CC with sodium channel dysfunction such as epilepsy, particularly
 CC generalised epilepsy with febrile seizures plus, malignant hyperthermia,
 CC myasthenia, episodic ataxia, neuropathic and inflammatory pain,
 CC Alzheimer's disease, Parkinson's disease, schizophrenia, hyperkplexia

CC and myotonia. Sequences ABG69289-ABG69293 represent human sodium channel
 CC alpha 1-subunit (SCN1A) polypeptides of the invention
 CC XX

Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 7.5e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTFFMMVWVIGNLVNLVNLFLALLSSSF 28
 Db 968 CLTFFMMVWVIGNLVNLVNLFLALLSSSF 995

RESULT 15

ABG69291 standard; protein; 2009 AA.

ABG69291;

21-OCT-2002 (first entry)

Human sodium channel alpha 1-subunit (SCN1A) variant protein #3.

Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
 generalised epilepsy with febrile seizures plus; myasthenia;
 sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
 inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
 schizophrenia; hyperkplexia; anticonvulsant; analgesic; neuroprotective;
 nootropic; anti-Parkinsonian; neuroleptic.

Homo sapiens.

WO200250096-A1.

27-JUN-2002.

20-DEC-2001; 2001WO-AU001648.

20-DEC-2000; 2000AU-00002203.

(BION-) BIONOMICS LTD.

Wallace RH, Mulley JC, Berkovic SF;

WPI; 2002-528445/56.

N-PADB; ABK98843.

New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
 gated sodium channel, useful for diagnosis of epilepsy, particularly
 generalized epilepsy with febrile seizures plus.

Claim 47; Page 107-117; 198pp; English.

The invention relates to a nucleic acid molecule encoding a mutant alpha
 subunit of a mammalian voltage-gated sodium channel. The DNA and the
 polypeptide may be used in the diagnosis of epilepsy, in particular
 CC generalised epilepsy with febrile seizures plus, and other disorders
 CC associated with sodium channel dysfunction. The polypeptide is useful for
 CC the screening of candidate pharmaceutical agents, where high throughput
 CC screening techniques are employed. The sequences are also useful in the
 CC manufacture of a medicament for the treatment of a disorder associated
 CC with sodium channel dysfunction such as epilepsy, particularly
 CC generalised epilepsy with febrile seizures plus, malignant hyperthermia,
 CC myasthenia, episodic ataxia, neuropathic and inflammatory pain,
 CC Alzheimer's disease, Parkinson's disease, schizophrenia, hyperkplexia
 CC and myotonia. Sequences ABG69289-ABG69293 represent human sodium channel
 CC alpha 1-subunit (SCN1A) polypeptides of the invention
 CC XX

Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 7.5e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTVFMVMVIGNLVNLFLALLSSSF 28
 |||||
 AC |||||
 XX |||||
 DB 968 CLTVFMVMVIGNLVNLFLALLSSSF 995

RESULT 16
 ABG69293
 ID ABG69293 standard; protein; 2009 AA.

AC ABG69293;
 XX
 DT 21-OCT-2002 (first entry)

DE Human sodium channel alpha 1-subunit (SCN1A) variant protein #5.

XX Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
 KW generalised epilepsy with febrile seizures plus; myasthenia;
 KW sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
 KW inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
 KW schizophrenia; hyperekplexia; anticonvulsant; analgesic; neuroprotective;
 KW nootropic; anti-Parkinsonian; neuroleptic.

XX Homo sapiens.

XX WO200250096-A1.

XX 27-JUN-2002.

XX 20-DEC-2001; 2001WO-AU001648.

XX 20-DEC-2000; 2000AU-00002203.

XX (BION-) BIONOMICS LTD.

PI Wallace RH, Mulley JC, Berkovic SF;

DR WPI; 2002-528445/56.

XX New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
 PT gated sodium channel, useful for diagnosis of epilepsy, particularly
 PT generalized epilepsy with febrile seizures plus.

PS Claim 53; Page 167-176; 1989pp; English.

XX The invention relates to a nucleic acid molecule encoding a mutant alpha
 CC subunit of a mammalian voltage-gated sodium channel. The DNA and the
 CC polypeptide may be used in the diagnosis of epilepsy, in particular
 CC generalised epilepsy with febrile seizures plus, and other disorders
 CC associated with sodium channel dysfunction. The polypeptide is useful for
 CC the screening of candidate pharmaceutical agents, where high throughput
 CC screening techniques are employed. The sequences are also useful in the
 CC manufacture of a medicament for the treatment of a disorder associated
 CC with sodium channel dysfunction such as epilepsy, particularly
 CC generalised epilepsy with febrile seizures plus, malignant hyperthermia,
 CC myasthenia, episodic ataxia, neuropathic and inflammatory pain.
 CC Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia
 CC and myotonia. Sequences ABG69289-ABG69293 represent human sodium channel
 CC alpha 1-subunit (SCN1A) polypeptides of the invention

XX Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;

Best Local Similarity 100.0%; Pred. No. 7.5e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTVFMVMVIGNLVNLFLALLSSSF 28
 |||||
 AC |||||
 XX |||||
 DB 968 CLTVFMVMVIGNLVNLFLALLSSSF 995

RESULT 17

ABG69289
 ID ABG69289 standard; protein; 2009 AA.
 XX
 AC ABG69289;
 XX
 DT 21-OCT-2002 (first entry)

DE Human sodium channel alpha 1-subunit (SCN1A) variant protein #1.

XX Human; sodium channel alpha 1-subunit; SCN1A; episodic ataxia; epilepsy;
 KW generalised epilepsy with febrile seizures plus; myasthenia;
 KW sodium channel dysfunction; malignant hyperthermia; neuropathic pain;
 KW inflammatory pain; Alzheimer's disease; Parkinson's disease; myotonia;
 KW schizophrenia; hyperekplexia; anticonvulsant; analgesic; neuroprotective;
 KW nootropic; anti-Parkinsonian; neuroleptic.

XX Homo sapiens.

XX WO200250096-A1.

XX 27-JUN-2002.

XX 20-DEC-2001; 2001WO-AU001648.

XX 20-DEC-2000; 2000AU-00002203.

XX (BION-) BIONOMICS LTD.

PI Wallace RH, Mulley JC, Berkovic SF;

DR WPI; 2002-528445/56.

DR N-PSDB; ABK98841.

XX New nucleic acid encoding mutant alpha subunit of a mammalian voltage-
 PT gated sodium channel, useful for diagnosis of epilepsy, particularly
 PT generalized epilepsy with febrile seizures plus.

PS Claim 36; Page 68-77; 1989pp; English.

XX The invention relates to a nucleic acid molecule encoding a mutant alpha
 CC subunit of a mammalian voltage-gated sodium channel. The DNA and the
 CC polypeptide may be used in the diagnosis of epilepsy, in particular
 CC generalised epilepsy with febrile seizures plus, and other disorders
 CC associated with sodium channel dysfunction. The polypeptide is useful for
 CC the screening of candidate pharmaceutical agents, where high throughput
 CC screening techniques are employed. The sequences are also useful in the
 CC manufacture of a medicament for the treatment of a disorder associated
 CC with sodium channel dysfunction such as epilepsy, particularly
 CC generalised epilepsy with febrile seizures plus, malignant hyperthermia,
 CC myasthenia, episodic ataxia, neuropathic and inflammatory pain.
 CC Alzheimer's disease, Parkinson's disease, schizophrenia, hyperekplexia
 CC and myotonia. Sequences ABG69289-ABG69293 represent human sodium channel
 CC alpha 1-subunit (SCN1A) polypeptides of the invention

XX Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 5; Length 2009;

Best Local Similarity 100.0%; Pred. No. 7.5e-18;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTVFMVMVIGNLVNLFLALLSSSF 28
 |||||
 AC |||||
 XX |||||
 DB 968 CLTVFMVMVIGNLVNLFLALLSSSF 995

RESULT 18
 ABG69290
 ID ABG69290 standard; protein; 2009 AA.

AC ABG69290;
 XX
 DT 21-OCT-2002 (first entry)

XX

FT Domain 803..821
 FT /label= Transmembrane_domain
 FT Domain 832..852
 FT /label= Transmembrane_domain
 FT Domain 893..911
 FT /label= Transmembrane_domain
 FT Binding-site 908..915
 FT /label= P loop
 FT /note= "ATP/GTP binding site"
 FT Domain 971..991
 FT /label= Transmembrane_domain
 FT Domain 1214..1482
 FT /note= "Ion transport protein domain"
 FT Domain 1251..1274
 FT /label= Transmembrane_domain
 FT Domain 1350..1369
 FT /label= Transmembrane_domain
 FT Domain 1459..1482
 FT /label= Transmembrane_domain
 FT Domain 1537..1785
 FT /note= "Ion transport protein domain"
 FT Domain 1543..1562
 FT /label= Transmembrane_domain
 FT Domain 1576..1594
 FT /label= Transmembrane_domain
 FT Domain 1602..1620
 FT /label= Transmembrane_domain
 FT Domain 1633..1650
 FT /label= Transmembrane_domain
 FT Domain 1673..1692
 FT /label= Transmembrane_domain
 FT Domain 1762..1785
 FT /label= Transmembrane_domain
 FT Binding-site 1916..1936
 FT /note= "IQ calmodulin-binding motif"
 FT WO200192304-A2.
 PN XX
 PD 06-DEC-2001.
 XX
 PD 25-MAY-2001; 2001WO-US017065.
 PF XX
 PR 26-MAY-2000; 2000US-0208424P.
 PR 01-JUN-2000; 2000US-0209001P.
 PR 08-JUN-2000; 2000US-0210588P.
 PR 16-JUN-2000; 2000US-0212335P.
 PR 22-JUN-2000; 2000US-0213747P.
 PR 29-JUN-2000; 2000US-0215391P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Thornton M, Wajia NK, Yue H, Nguyen DB, Lai P, Gandhi AR,
 PI Tribouley CM, Yao MG, Ramkumar J, Au-Young J, Lu Y, Tang YT,
 PI Azimzai Y, Bruns CM, Griffin JA, Yang J, Sanjanwala MS, Raumann BE,
 PI Lee EA, Hafalia A, Baughn MR, Green BD, Khan FA, Kearney LJ,
 PI Ellicot VS, Seihamer JJ, Policky JL, Borowsky ML, Burford N, Ding L,
 PI Lu DM, Hillman JL;
 XX
 XX WPI; 2002-122055/16.
 DR N-PSDB; AAD27266.
 XX
 PT New human transporters and ion channels (TRICH) polypeptides useful for
 PT diagnosing, treating or preventing disorders associated with aberrant
 PT expression of TRICH.
 XX
 XX Claim 1; Page 158-162; 210pp; English.
 XX
 XX The invention relates to human transporters and ion channels (TRICH)
 CC polypeptides and their cDNA molecules. The nucleic acid and polypeptide
 CC sequences are useful in the diagnosis, treatment, and prevention of
 CC disorders associated with transport (akinesia, cystic fibrosis, Bell's
 CC palsy, amyotrophic lateral sclerosis); neurological (Alzheimer's disease,
 CC amnesia, dementia); muscle (cardiomyopathy, myocarditis, Duchenne's

CC muscular dystrophy); immunological (AIDS, Addison's disease, allergies,
 CC asthma); cell proliferative disorders (cancers, leukaemia, psoriasis);
 CC cardiac disease (angina, hypertension, or bradyarrhythmia) and in the
 CC assessment of the effects of exogenous compounds on the expression of
 CC nucleic acid and amino acid sequences of transporters and ion channels.
 CC The polynucleotides may be used to detect and quantify gene expression in
 CC biopsied tissues in which TRICH expression may be correlated with a
 CC disease, to generate hybridization probes for mapping naturally occurring
 CC genomic sequence, and in drug screening. The present sequence is human
 CC TRICH-13 protein
 XX
 XX SQ Sequence 2009 AA;
 XX
 XX Query Match 100.0%; Score 28; DB 5; Length 2009;
 XX Best Local Similarity 100.0%; Pred. No. 7.5e-18;
 XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CLTVFMVMVIGNIVLNLFLALLISF 28
 Db 968 CLTVFMVMVIGNIVLNLFLALLISF 995
 XX
 XX RESULT 21
 XX ADB78599
 XX ID ADB78599 standard; protein; 2009 AA.
 XX
 XX AC ADB78599;
 XX
 XX DT 04-DEC-2003 (first entry)
 XX
 XX DE Human sodium channel subunit mutant SEQ ID NO:143.
 XX
 XX KW mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
 KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.
 XX
 XX OS Synthetic.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO2003008574-A1.
 XX
 XX PD 30-JAN-2003.
 XX
 XX PF 08-JUL-2002; 2002WO-AU000910.
 XX
 XX PR 18-JUL-2001; 2001AU-00006452.
 XX PR 05-MAR-2002; 2002AU-00000910.
 XX PR 13-MAY-2002; 2002AU-00002292.
 XX
 XX PA (BION-) BIONOMICS LTD.
 XX PA (WALL/) WALLACE R W.
 XX
 XX PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
 XX PI Berkovic SF, Scheffer IE;
 XX
 XX WPI; 2003-239332/23.
 DR N-PSDB; ADB78638.
 XX
 XX PT Identifying predisposition to an ion channel dysfunction, such as
 XX PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 XX PT schizophrenia, anxiety and depression, by detecting encoding-gene
 XX PT mutation events.
 XX
 XX PS Claim 13; SEQ ID NO 143; 106pp; English.
 XX
 XX The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,

CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephrotoxic, antidiabetic, and
 CC ion channel activator. A polynucleotide of the invention acts as an
 CC nucleic acid, polypeptide, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemia, periodic paralysis, myotonia, malignant hyperthermia,
 CC disease, Parkinson's disease, episodic ataxia, migraine, Alzheimer's
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 7; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 7.5e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTFFMMVWVIGNLVVLNLFALLLSF 28
 DB 968 CLTFFMMVWVIGNLVVLNLFALLLSF 995

RESULT 22

ADB78595
 ADB78595 standard; protein; 2009 AA.

XX ADB78595;
 XX 04-DEC-2003 (first entry)

DE Human sodium channel subunit mutant SEQ ID NO:139.

XX mutagen; mutant; ion channel; ion channel subunit; ICS; nootropic;
 KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.

OS Synthetic.

XX Homo sapiens.

XX WO2003008574-A1.

XX 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.

XX 18-JUL-2001; 2001AU-00006452.

XX 05-MAR-2002; 2002AU-0000910.

XX 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

XX (WALL/) WALLACE R W.

XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
 XX Berkovic SF, Scheffer IE;

XX WPI; 2003-239332/23.

PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.

XX Claim 13; SEQ ID NO 139; 106bp; English.

XX The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antimigraine, analgesic, nephrotoxic, antiparkinsonian,
 CC neuroleptic, tranquiliser, antidepressant, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The method, isolated
 CC nucleic acid, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemia, periodic paralysis, myotonia, malignant hyperthermia,
 CC disease, Parkinson's disease, episodic ataxia, migraine, Alzheimer's
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 2009 AA;

Query Match 100.0%; Score 28; DB 7; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 7.5e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTFFMMVWVIGNLVVLNLFALLLSF 28
 DB 968 CLTFFMMVWVIGNLVVLNLFALLLSF 995

RESULT 23

ADB78593
 ADB78593 standard; protein; 2009 AA.

XX ADB78593;
 XX 04-DEC-2003 (first entry)

DE Human sodium channel subunit mutant SEQ ID NO:137.

XX mutagen; mutant; ion channel; ion channel subunit; ICS; nootropic;
 KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
 KW ion channel dysfunction; human.

OS Synthetic.

XX Homo sapiens.

XX WO2003008574-A1.

XX 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.

XX 18-JUL-2001; 2001AU-00006452.

XX 05-MAR-2002; 2002AU-0000910.

XX 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

XX (WALL/) WALLACE R W.

XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;
 XX
 XX WPI; 2003-239332/23.
 DR N-PSDB; ADB78632.
 DR
 PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 137; 106pp; English.
 XX
 XX The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephroprotective, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 CC
 XX
 SQ Sequence 2009 AA;
 Query Match 100.0%; Score 28; DB 7; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 7.5e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTMMWVYIGNLVNLFALLSSSF 28
 Db 968 CTTTMMWVYIGNLVNLFALLSSSF 995
 RESULT 24
 ADB78594 standard; protein; 2009 AA.
 XX
 AC ADB78594;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human sodium channel subunit mutant SEQ ID NO:138.
 XX
 XX mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
 KM neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KM antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KM nephroprotective; antidiabetic; ophthalmological; epilepsy;
 KM ion channel dysfunction; human.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN W02003008574-A1.
 XX
 PD 30-JAN-2003.
 XX
 PF 08-JUL-2002; 2002WO-AU000910.

XX
 PR 18-JUL-2001; 2001AU-00006452.
 PR 05-MAR-2002; 2002AU-00000910.
 PR 13-MAY-2002; 2002AU-00002292.
 XX
 XX (BION-) BIONOMICS LTD.
 PA (WALL) WALLACE R W.
 PA
 PI Mulvey JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
 PI Berkovic SF, Scheffer IE;
 XX
 XX WPI; 2003-239332/23.
 DR N-PSDB; ADB78633.
 DR
 PT Identifying predisposition to an ion channel dysfunction, such as
 PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 138; 106pp; English.
 XX
 XX The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
 CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephroprotective, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonias, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 CC
 XX
 SQ Sequence 2009 AA;
 Query Match 100.0%; Score 28; DB 7; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 7.5e-18;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTTMMWVYIGNLVNLFALLSSSF 28
 Db 968 CTTTMMWVYIGNLVNLFALLSSSF 995
 RESULT 25
 ADB78598 standard; protein; 2009 AA.
 XX
 AC ADB78598;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human sodium channel subunit mutant SEQ ID NO:142.
 XX
 XX mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
 KM neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
 KM antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
 KM nephroprotective; antidiabetic; ophthalmological; epilepsy;
 KM ion channel dysfunction; human.

```

XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO2003008574-A1.
XX PD 30-JAN-2003.
XX PF 08-JUL-2002; 2002WO-AU000910.
XX PR 18-JUL-2001; 2001AU-00006452.
XX PR 05-MAR-2002; 2002AU-00000910.
XX PR 13-MAY-2002; 2002AU-00002292.
XX PA (BION-) BIONOMICS LTD.
XX PA (WALL/) WALLACE R W.
XX PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE,
XX PI Berkovic SF, Scheffer IE,
XX DR MPI; 2003-239332/23.
XX DR N-PSDB; ADB78637.
XX PT Identifying predisposition to an ion channel dysfunction, such as
XX PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
XX PT schizophrenia, anxiety and depression, by detecting encoding-gene
XX PT mutation events.
XX PS Claim 13; SEQ ID NO 142; 106bp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has nootropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonia, malignant hyperthermia,
CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 2009 AA:

```

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Query Match      100.0%; Score 28; DB 7; Length 2009;
Best Local Similarity 100.0%; Pred. No. 7.5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTTTFFMMVMTVIGNVLVNLFFALLISSF 28
   ||| ||| ||| ||| ||| ||| ||| |||
Db 968 CTTTFFMMVMTVIGNVLVNLFFALLISSF 995

```

Search completed: January 27, 2005, 17:45:15
 Job time : 88.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:05 ; Search time 17 Seconds
(without alignments)
158.475 Million cell updates/sec

Title: US-10-608-584-13

Perfect score: 28

Sequence: 1 CLTVFMVMVIGNLVNLFLALLLSF 28

Scoring table: OLIGO

Searched: 283416 seqs, 96216763 residues

Word size: 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database: PIR_79:*

1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	200	2	148108 sodium channel alp
2	28	100.0	2005	2	A46269 sodium channel alp
3	28	100.0	2005	2	B25019 sodium channel pro
4	25	89.3	1976	2	I56555 sodium channel alp
5	23	82.1	1977	2	S54771 sodium channel alp
6	22	78.6	1835	2	I54323 sodium channel alp
7	22	78.6	1836	2	I54893 sodium channel alp
8	22	78.6	1836	2	U50648 sodium channel alp
9	22	78.6	1836	2	I51964 sodium channel alp
10	22	78.6	1840	1	CHRTM1 sodium channel pro
11	21	75.0	1951	2	S00320 sodium channel pro
12	21	75.0	1983	2	A60054 sodium channel pro
13	21	75.0	2016	2	A38195 sodium channel pro
14	21	75.0	2019	2	A33966 sodium channel pro
15	18	64.3	1784	2	I43167 sodium channel pro
16	17	60.7	109	2	S72488 sodium channel pro
17	17	60.7	1034	2	S60051 sodium channel alp
18	17	60.7	1034	2	S60060 sodium channel alp
19	17	60.7	1034	2	S72467 sodium channel alp
20	17	60.7	1820	2	A33299 sodium channel pro
21	17	60.7	1993	2	T30902 sodium channel pro
22	17	60.7	2049	2	T43161 sodium channel pro
23	17	60.7	2049	2	S72458 sodium channel pro
24	16	57.1	2009	2	A25019 sodium channel pro
25	14	50.0	1695	2	J50084 voltage-gated sodi
26	12	42.9	1820	1	CHBE sodium channel pro
27	11	39.3	1739	2	A48298 sodium channel hom
28	10	35.7	1321	2	A60165 sodium channel pro
29	10	35.7	1810	2	T31092 probable voltage-g

30	9	32.1	409	2	F89834 hypothetical prote
31	8	32.1	1957	2	S68453 sodium channel pro
32	8	28.6	501	2	I61512 TNF receptor assoc
33	8	28.6	616	2	AF0263 proteinase IV (EC
34	8	28.6	1699	2	T31340 voltage-gated sodi
35	7	25.0	33	2	A36154 benzphetamine N-de
36	7	25.0	68	2	S49412 fibrinogen-binding
37	7	25.0	100	2	S66718 probable membr
38	7	25.0	101	2	S60632 NADH2 dehydrogen
39	7	25.0	104	1	PFHUA4 platelet factor 4
40	7	25.0	116	2	B89887 hypothetical prote
41	7	25.0	118	2	S42598 hypothetical prote
42	7	25.0	155	2	S60647 NADH2 dehydrogen
43	7	25.0	166	2	JC6559 interferon-gamma p
44	7	25.0	183	2	E72459 hypothetical prote
45	7	25.0	218	2	T19256 hypothetical prote
46	7	25.0	237	2	AF0772 probable exported
47	7	25.0	247	2	B86161 F1003.11 protein -
48	7	25.0	257	2	H84597 hypothetical prote
49	7	25.0	292	2	A47125 transcription acti
50	7	25.0	358	2	T26231 hypothetical prote
51	7	25.0	386	2	AH3467 glycine betaine/1-
52	7	25.0	390	2	H70904 probable lpxr prot
53	7	25.0	420	2	T39523 probable transmem
54	7	25.0	451	2	H89798 conserved hypothet
55	7	25.0	480	2	G70302 conserved hypothet
56	7	25.0	505	2	AC1469 internalin like pr
57	7	25.0	513	2	A71004 hypothetical prote
58	7	25.0	538	2	G72539 probable CTP synth
59	7	25.0	578	2	AH1020 cyclochrome c-type
60	7	25.0	721	2	F87611 TonB-dependent rec
61	7	25.0	1158	2	S57348 nuclear factor RIP
62	7	25.0	1172	2	T36053 probable ABC-type
63	7	25.0	1438	2	B71610 Wd40 WEB-1 homolog
64	7	25.0	1582	2	A56248 sulfonylurea recep
65	7	25.0	1765	2	T42368 sodium channel alp
66	6	21.4	52	2	B96798 hypothetical prote
67	6	21.4	66	2	C97928 hypothetical prote
68	6	21.4	73	2	B83338 hypothetical prote
69	6	21.4	83	2	T03673 pili protein (clon
70	6	21.4	85	2	H83492 hypothetical prote
71	6	21.4	97	2	B95038 preprotein translo
72	6	21.4	97	2	H97908 conserved hypothet
73	6	21.4	100	1	F70309 protein export mem
74	6	21.4	102	2	C86365 probable 10kd chap
75	6	21.4	102	2	A75417 hypothetical prote
76	6	21.4	103	2	C71189 hypothetical prote
77	6	21.4	107	2	F71700 hypothetical prote
78	6	21.4	111	2	B70035 chaperonin homolog
79	6	21.4	117	2	AG3451 murein hydrolase e
80	6	21.4	120	2	S57057 probable membrane
81	6	21.4	123	2	A75273 hypothetical prote
82	6	21.4	123	2	T35812 probable small hyd
83	6	21.4	138	2	AD1850 hypothetical prote
84	6	21.4	139	2	B69744 hypothetical prote
85	6	21.4	149	2	F75327 hypothetical prote
86	6	21.4	158	2	C82494 conserved hypothet
87	6	21.4	164	2	S22204 photosystem I chai
88	6	21.4	165	2	B75502 hypothetical prote
89	6	21.4	166	1	IYBOG interferon gamma p
90	6	21.4	166	2	S12723 interferon gamma p
91	6	21.4	167	2	S35795 androgen receptor
92	6	21.4	167	2	D75636 hypothetical prote
93	6	21.4	175	2	B95412 hypothetical prote
94	6	21.4	178	2	C72025 conserved hypothet
95	6	21.4	178	2	A86598 C718 hypothetical
96	6	21.4	180	2	T15426 hypothetical prote
97	6	21.4	184	2	T38152 hypothetical RBR1-
98	6	21.4	184	2	AB2503 hypothetical prote
99	6	21.4	185	2	T24345 hypothetical prote
100	6	21.4	185	2	S76706 hypothetical prote

ALIGNMENTS

RESULT 1

I48108

Sodium channel alpha subunit - long-tailed hamster (fragment)

C:Species: Cricetus longicaudatus (long-tailed hamster)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C:Accession: I48108

R:Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.

Am. J. Physiol. 264, 803-809, 1993

A:Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster

A:Reference number: I48107

A:Accession: I48108

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-200 <RES>

A:Cross-references: UNIPROT:Q60464; GB:M87541; NID:g191069; PIDN:AAA36979.1; PID:G553840

A:Gene: CNOL

C:Superfamily: sodium channel protein

C:Keywords: duplication

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 200;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CLTVFMVWVIGNLVNLFLALLSSSF 28

45 CLTVFMVWVIGNLVNLFLALLSSSF 72

RESULT 2

A46269

Sodium channel alpha chain HBA - human

C:Species: Homo sapiens (man)

C>Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997

C:Accession: A46269

R:Ahmed, C.M.; Ware, D.H.; Lee, S.C.; Patten, C.D.; Ferrer-Montiel, A.V.; Schinder, A.F.

Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992

A:Title: Primary structure, chromosomal localization, and functional expression of a vol

A:Reference number: A46269; MUID:92290418; PMID:1325650

A:Accession: A46269

A:Molecule type: mRNA

A:Residues: 1-2005 <AHM>

A:Cross-references: GB:M94055

A:Experimental source: brain

A:Note: sequence extracted from NCBI backbone (NCBIF:113082)

C:Genetics:

A:Map position: 2q23-q24.3

C:Superfamily: sodium channel protein

C:Keywords: duplication

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 2005;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CLTVFMVWVIGNLVNLFLALLSSSF 28

959 CLTVFMVWVIGNLVNLFLALLSSSF 986

RESULT 3

B25019

Sodium channel protein II - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C:Accession: B25019; S24804

R:Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takehana, H.; Kurasaki, M.; Takahashi, H.

Nature 320, 188-192, 1986

A:Title: Existence of distinct sodium channel messenger RNAs in rat brain.

A:Reference number: A93377; MUID:86146901; PMID:3754035

A:Accession: B25019

Query Match

Best Local Similarity 100.0%; Score 23; DB 2; Length 1977;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 VFMVWVIGNLVNLFLALLSSSF 28

952 VFMVWVIGNLVNLFLALLSSSF 976

RESULT 4

I56555

Sodium channel protein 6 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I56555

R:Schaller, K.L.; Krzemien, D.M.; Yarowsky, P.J.; Krueger, B.K.; Caldwell, J.H.

J. Neurosci. 15, 3231-3242, 1995

A:Title: A novel, abundant sodium channel expressed in neurons and glia.

A:Reference number: I56555; MUID:95271284; PMID:7751906

A:Accession: I56555

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1976 <RES>

A:Cross-references: UNIPROT:Q63541; GB:L39018; NID:g829033; PIDN:AA642059.1; PID:g829034

A:Gene: SC26

C:Superfamily: sodium channel protein

C:Keywords: duplication

Query Match

Best Local Similarity 100.0%; Score 25; DB 2; Length 1976;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 VFMVWVIGNLVNLFLALLSSSF 28

952 VFMVWVIGNLVNLFLALLSSSF 976

RESULT 5

S54771

Sodium channel alpha subunit - human

C:Species: Homo sapiens (man)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C:Accession: S54771

R:Klugbauer, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.

EMBO J. 14, 1084-1090, 1995

A:Title: Structure and functional expression of a new member of the tetrodotoxin-sensitive

A:Reference number: S54771; MUID:95237189; PMID:7720699

A:Accession: S54771

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1977 <KLU>

A:Cross-references: UNIPROT:Q15858; EMBL:X82835; NID:g758109; PIDN:CAA58042.1; PID:g7581

C:Superfamily: sodium channel protein

C:Keywords: duplication

Query Match

Best Local Similarity 100.0%; Score 23; DB 2; Length 1977;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 VFMVWVIGNLVNLFLALLSSSF 28

952 VFMVWVIGNLVNLFLALLSSSF 976

Best Local Similarity 100.0%; Pred. No. 1,2e-13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 MMVIGNLVVLNLFALLLSF 28
Db 938 MMVIGNLVVLNLFALLLSF 960

RESULT 6
154323
sodium channel alpha subunit - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C:Accession: 154323
R:McClatchey, A.I.; Lin, C.S.; Wang, J.; Hoffman, E.P.; Rojas, C.; Gussella, J.F.
Hum. Mol. Genet. 1, 521-527, 1992
A:Title: The genomic structure of the human skeletal muscle sodium channel gene.
A:Reference number: 154323; MUID:9338444; PMID:1339144
A:Accession: 154323
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1835 <RES>
A:Cross-references: GB:L01963; NID:G337992; PIDN:AAA75557.1; PID:G908809
C:Genetics:
A:Gene: GDB:SCN4A
A:Cross-references: GDB:125181; OMIM:170500
A:Map position: 17q23.1-17q25.3
A:Insertions: 913; 1312; 1612; 2042; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3; 6
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query March 78.6%; Score 22; DB 2; Length 1835;
Best Local Similarity 100.0%; Pred. No. 9,7e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MMVIGNLVVLNLFALLLSF 28
Db 784 MMVIGNLVVLNLFALLLSF 805

RESULT 7
164893
sodium channel alpha subunit - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: 164893
R:George, A.L.
Ann. Neurol. 31, 131-137, 1992
A:Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium c
A:Reference number: 151964; MUID:92246457; PMID:1315496
A:Accession: 164893
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1836 <RES>
A:Cross-references: UNIPROT:P35499; GB:M81758; NID:G338212; PIDN:AAA60554.1; PID:G338213
C:Genetics:
A:Gene: SKM1
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query March 78.6%; Score 22; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 9,7e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MMVIGNLVVLNLFALLLSF 28
Db 784 MMVIGNLVVLNLFALLLSF 805

RESULT 8
US0648
sodium channel alpha chain - human
C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: US0648; A42099
R:Wang, J.; Rojas, C.V.; Zhou, J.; Schwartz, L.S.; Nicholas, H.; Hoffmann, E.P.
Biochem. Biophys. Res. Commun. 182, 794-801, 1992
A:Title: Sequence and genomic structure of the human adult skeletal muscle sodium channe
A:Reference number: US0648; MUID:92134303; PMID:1310396
A:Accession: US0648
A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA
A:Residues: 1-1836 <MAN>
A:Cross-references: UNIPROT:P35499
A>Note: 861 Asp was also found as the result of polymorphism
R:McClatchey, A.I.; Van den Berg, P.; Perlick-Vance, M.A.; Kaskind, W.; Verjellen, C.; M
Cell 68, 769-774, 1992
A:Title: Temperature-sensitive mutations in the III-IV cytoplasmic loop region of the sk
A:Reference number: A42099; MUID:92154689; PMID:1310898
A:Accession: A42099
A:Molecule type: DNA
A:Residues: 1299-1351 <MCC>
A:Cross-references: GB:S82622; NID:G245611; PIDN:AA821450.1; PID:G245612
A:Experimental source: skeletal muscle
A>Note: sequence extracted from NCBI backbone (NCBI:82622, NCBI:82623)
C:Genetics:
A:Gene: GDB:SCN4A
A:Cross-references: GDB:125181; OMIM:170500
A:Map position: 17q23.1-17q25.3
C:Superfamily: sodium channel protein
C:Keywords: duplication; glycoprotein; phosphoprotein; transmembrane protein

F:112-150/Domain: transmembrane #status predicted <TR1>
F:115-178/Domain: transmembrane #status predicted <TR2>
F:191-210/Domain: transmembrane #status predicted <TR3>
F:217-236/Domain: transmembrane #status predicted <TR4>
F:253-266/Domain: transmembrane #status predicted <TR5>
F:424-449/Domain: transmembrane #status predicted <TR6>
F:574-597/Domain: transmembrane #status predicted <R11>
F:609-632/Domain: transmembrane #status predicted <R12>
F:641-660/Domain: transmembrane #status predicted <R13>
F:667-686/Domain: transmembrane #status predicted <R14>
F:702-724/Domain: transmembrane #status predicted <R15>
F:777-802/Domain: transmembrane #status predicted <R16>
F:1027-1049/Domain: transmembrane #status predicted <R11>
F:1064-1089/Domain: transmembrane #status predicted <R12>
F:1096-1116/Domain: transmembrane #status predicted <R13>
F:1122-1143/Domain: transmembrane #status predicted <R14>
F:1163-1184/Domain: transmembrane #status predicted <R15>
F:1269-1295/Domain: transmembrane #status predicted <R16>
F:1349-1372/Domain: transmembrane #status predicted <R11>
F:1384-1407/Domain: transmembrane #status predicted <R12>
F:1414-1437/Domain: transmembrane #status predicted <R13>
F:1447-1469/Domain: transmembrane #status predicted <R14>
F:1485-1507/Domain: transmembrane #status predicted <R15>
F:1574-1596/Domain: transmembrane #status predicted <R16>
F:121,149,220,378,415,1019,1130,1242,1313,1721,1826/Binding site: phosphate (Thr) (covalen
F:156,251,513,653,1511,1746/Binding site: phosphate (Ser) (covalent) (by protein kinase A
F:214,268,591,297,303,315,333,362,501,702,961,1191,1205/Binding site: carboxylate (by
F:246,670,725,850,950,1127,1195,1328/Binding site: phosphate (Ser) (covalent) (by protei
F:387,457/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predict

Query March 78.6%; Score 22; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 9,7e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 MMVIGNLVVLNLFALLLSF 28
Db 784 MMVIGNLVVLNLFALLLSF 805

RESULT 9
151964
sodium channel alpha chain SCN4A, skeletal muscle - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C:Accession: 151964

R,George, A.L.
 Ann. Neurol. 31, 131-137, 1992
 A>Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium C
 A:Reference number: 151964; MUID:92246457; PMID:1315496
 A:Accession: 151964
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1836 <RES>
 A:Cross-references: UNIPROT:P35499; GB:L04236; NID:G292485; PIDN:AA59624.1; PID:G292487
 A:Gene: GDB:SCN4A
 A:Cross-references: GDB:125181; OMIM:170500
 A:Map position: 17q23.1-17q25.3
 A:Introns: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3; 6
 C:Superfamily: sodium channel protein
 C:Keywords: duplication; skeletal muscle

Query Match 78.6%; Score 22; DB 2; Length 1836;
 Best Local Similarity 100.0%; Pred. No. 9.7e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 MWVIGNLVNLFLALLSSP 28
 |||||
 Db 784 MWVIGNLVNLFLALLSSP 805

RESULT 10
 CHRTM1
 sodium channel protein mul alpha chain, skeletal muscle - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
 C:Accession: JN0007
 R:Timer: J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.; Kall
 Neuron 3, 33-49, 1998
 A>Title: Primary structure and functional expression of a mammalian skeletal muscle sodi
 A:Reference number: JN0007; MUID:90148778; PMID:2559760
 A:Accession: JN0007
 A:Molecule type: mRNA
 A:Residues: 1-1840 <TRI>
 A:Cross-references: UNIPROT:P15390; GB:M26643; NID:G205651; PIDN:AAA1682.1; PID:G205652
 C:Comment: Action potentials propagated by skeletal muscle sodium channels are responsi
 C:Comment: This heavily glycosylated protein contains four homologous domains, each of w
 C:Superfamily: sodium channel protein
 C:Keywords: duplication; glycoprotein; ion transport; neuromuscular junction; phosphop
 F:120-458,561-813,1013-1305,1335-1611/region: duplication
 F:56,251,1321,1504/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #
 F:214,286,291,297,303,309,315,327,356,502,696,954,1184,1198,1563,1702/Binding site: cat

Query Match 78.6%; Score 22; DB 1; Length 1840;
 Best Local Similarity 100.0%; Pred. No. 9.7e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 MWVIGNLVNLFLALLSSP 28
 |||||
 Db 778 MWVIGNLVNLFLALLSSP 799

RESULT 11
 S00320
 sodium channel protein III - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C:Accession: S00320
 R:Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S.
 FEBS Lett. 228, 187-194, 1988
 A>Title: Primary structure of rat brain sodium channel III deduced from the cDNA sequenc
 A:Reference number: S00320; MUID:88137594; PMID:2449363
 A:Accession: S00320
 A:Molecule type: mRNA
 A:Residues: 1-1951 <RAY>
 A:Cross-references: UNIPROT:P08104; EMBL:Y00766; NID:957210; PIDN:CAA68735.1; PID:957211
 A>Note: 270-Ile, 278-Leu, 355-Thr, 513-Lys, and 1059-Arg were also found

C:Superfamily: sodium channel protein
 C:Keywords: duplication; transmembrane protein

Query Match 75.0%; Score 21; DB 2; Length 1951;
 Best Local Similarity 100.0%; Pred. No. 8.9e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 MWVIGNLVNLFLALLSSP 28
 |||||
 Db 918 MWVIGNLVNLFLALLSSP 938

RESULT 12
 A60054
 sodium channel protein IIb, long form - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
 C:Accession: A60054; B44824
 R:Joho, R.H.; Moorman, J.R.; Vandongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster, C
 Brain Res. Mol. Brain Res. 7, 105-113, 1990
 A>Title: Toxin and kinetic profile of rat brain type III sodium channels expressed in Xer
 A:Reference number: A60054; MUID:90251117; PMID:2160038
 A:Accession: A60054
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1983 <JOH>
 A:Cross-references: UNIPROT:Q64243
 R:Schaller, K.L.; Kremien, D.M.; McKenna, N.M.; Caldwell, J.H.
 J. Neurosci. 12, 1370-1381, 1992
 A>Title: Alternatively spliced sodium channel transcripts in brain and muscle.
 A:Reference number: A44824; MUID:92211397; PMID:1313493
 A:Accession: B44824
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 611-662 <SCH>
 A:Cross-references: GB:S97388; NID:G248225; PIDN:AA821984.1; PID:G248226
 A:Experimental source: skeletal muscle
 A>Note: sequence inconsistent with the nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBIN:97388, NCBI:P:97391)
 C:Superfamily: sodium channel protein
 C:Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane prote

Query Match 75.0%; Score 21; DB 2; Length 1983;
 Best Local Similarity 100.0%; Pred. No. 9e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 MWVIGNLVNLFLALLSSP 28
 |||||
 Db 950 MWVIGNLVNLFLALLSSP 970

RESULT 13
 A38195
 sodium channel protein hH, cardiac - human
 N:Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-I NaC
 C:Species: Homo sapiens (man)
 C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A38195
 R:Gellens, M.E.; George Jr., A.L.; Chen, L.O.; Chahine, M.; Horn, R.; Barchi, R.L.; Kall
 Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
 A>Title: Primary structure and functional expression of the human cardiac tetrodotoxin-I
 A:Reference number: A38195; MUID:92115699; PMID:11309946
 A:Accession: A38195
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-2016 <GEL>
 A:Cross-references: UNIPROT:Q14524; GB:M77235; NID:G184038; PIDN:AAA5644.1; PID:G184039
 A:Experimental source: heart
 C:Superfamily: sodium channel protein
 C:Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium chan
 Query Match 75.0%; Score 21; DB 2; Length 2016;
 Best Local Similarity 100.0%; Pred. No. 9.2e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VMVIGNLVVNLFLALLLSF 28
 |||||
 Db 922 VMVIGNLVVNLFLALLLSF 942

RESULT 14

A33996 sodium channel protein I, cardiac - rat

N.Alternate names: sodium channel protein (SKM2) alpha chain

C.Species: Rattus norvegicus (Norway rat)

C.Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004

C.Accession: A33996; J00412

R.Rogart, R.B.; Cribbs, L.L.; Muglia, L.K.; Kephart, D.D.; Kaiser, M.W.

Proc. Natl. Acad. Sci. U.S.A. 86, 8170-8174, 1989

A.Title: Molecular cloning of a putative tetrodotoxin-resistant rat heart Na(+) channel

A.Reference number: A33996; MUID:90046760; PMID:2554302

A.Accession: A33996

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-2019 <ROS>

A.Cross-references: UNIPROT:P15389; GB:M27902; NID:G206857; PIDN:AAA2114.1; PID:G206858

R.Kallen, R.G.; Sheng, Z.H.; Yang, J.; Chen, L.; Rogart, R.B.; Barchi, R.L.

Neuron 4, 233-242, 1990

A.Title: Primary structure and expression of a sodium channel characteristic of denervat

A.Reference number: J00412; MUID:90166613; PMID:2155010

A.Accession: J00412

A.Molecule type: mRNA

A.Residues: 1-479, 481-1712, 'T', 1714-1963, 'R', 1965-2019 <KAL>

A.Experimental source: muscle

C.Superfamily: sodium channel protein

C.Keywords: cardiac muscle; duplication; heart; sodium channel; transmembrane protein

Query Match 75.0%; Score 21; DB 2; Length 2019;

Best Local Similarity 100.0%; Pred. No. 9.2e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VMVIGNLVVNLFLALLLSF 28
 |||||
 Db 925 VMVIGNLVVNLFLALLLSF 945

RESULT 15

T43167 sodium channel protein - California market squid

C.Species: Loligo opalescens (California market squid)

C.Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C.Accession: T43167

R.Rosenthal, J.J.; Gilly, W.F.

Proc. Natl. Acad. Sci. U.S.A. 90, 10026-10030, 1993

A.Title: Amino acid sequence of a putative sodium channel expressed in the giant axon of

A.Reference number: Z22324; MUID:94052096; PMID:8234251

A.Accession: T43167

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-1784 <ROS>

A.Cross-references: UNIPROT:Q25377; EMBL:L19979; NID:G349118; PID:G349119; PIDN:AAA16202

A.Experimental source: stellate ganglia

C.Superfamily: sodium channel protein

C.Keywords: ion transport; membrane protein; sodium channel; voltage-gated ion channel

Query Match 64.3%; Score 18; DB 2; Length 1784;

Best Local Similarity 100.0%; Pred. No. 5.5e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 IGNTLVVNLFLALLLSF 28
 |||||
 Db 799 IGNTLVVNLFLALLLSF 816

RESULT 16

S72488

sodium channel protein para-type alpha chain - house fly (strain SBO) (fragment)

C.Species: Musca domestica (house fly)

A.Variety: strain SBO

C.Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004

C.Accession: S72488

R.Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.

Mol. Gen. Genet. 252, 61-68, 1996

A.Title: Cloning and sequencing of the para-type sodium channel gene from susceptible an

A.Reference number: S72487; MUID:96397510; PMID:8804404

A.Accession: S72488

A.Status: not compared with conceptual translation

A.Molecule type: mRNA

A.Residues: 1-109 <MT>

A.Cross-references: UNIPROT:Q25439; UNIPROT:Q25440; UNIPROT:Q254615; UNIPROT:Q254617

A.Experimental source: strain SBO

C.Superfamily: sodium channel protein

C.Keywords: sodium channel; transmembrane protein

Query Match 60.7%; Score 17; DB 2; Length 109;

Best Local Similarity 100.0%; Pred. No. 4.3e-09;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VIGNLVVNLFLALLLS 26
 |||||
 Db 71 VIGNLVVNLFLALLLS 87

RESULT 17

S60051 sodium channel alpha chain, exon c-containing splice form - fruit fly (Drosophila virilis)

C.Species: Drosophila virilis

C.Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004

C.Accession: S60051

R.Thackeray, J.R.; Ganetzky, B.

Genetics 141, 203-214, 1995

A.Title: Conserved alternative splicing patterns and splicing signals in the Drosophila

A.Reference number: S60051; MUID:96042905; PMID:8536968

A.Accession: S60051

A.Status: nucleic acid sequence not shown

A.Molecule type: nucleic acid

A.Residues: 1-1034 <THA>

A.Cross-references: UNIPROT:Q24714; EMBL:U26343

C.Genetics:

A.Gene: FLYBase:FlyBase:FBgn0015214

A.Cross-references: FlyBase:FBgn0015214

C.Superfamily: sodium channel protein

C.Keywords: alternative splicing; duplication; transmembrane protein

F.306-329/Region: alternatively spliced segment 1 (exon 4) #status experimental

F.330-350/Region: alternatively spliced segment a #status experimental

F.538-545/Region: alternatively spliced segment b (exon 9) #status experimental

F.874-886/Region: alternatively spliced segment c (exon 12) #status experimental

F.887-896/Region: alternatively spliced segment d (exon 13) #status experimental

F.958-982/Region: alternatively spliced segment h (exon 14) #status experimental

Query Match 60.7%; Score 17; DB 2; Length 1034;

Best Local Similarity 100.0%; Pred. No. 3e-08;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VIGNLVVNLFLALLLS 26
 |||||
 Db 800 VIGNLVVNLFLALLLS 816

RESULT 18

S60060

sodium channel alpha chain, exon d-containing splice form - fruit fly (Drosophila virilis)

C.Species: Drosophila virilis

C.Date: 24-Aug-1996 #sequence_revision 08-Nov-1996 #text_change 09-Jul-2004

C.Accession: S60060

R.Thackeray, J.R.; Ganetzky, B.

Genetics 141, 203-214, 1995

A.Title: Conserved alternative splicing patterns and splicing signals in the Drosophila

A.Reference number: S60051; MUID:96042905; PMID:8536968

A:Accession: S60060
 A:Status: nucleic acid sequence not shown
 A:Molecule type: nucleic acid
 A:Residues: 1-1034 <THA>
 A:Cross-references: UNIPROT:Q24714; EMBL:U26343
 C:Genetics:
 A:Gene: FlyBase:FlyBase:FBgn0015214
 C:Superfamily: sodium channel protein
 C:Keywords: alternative splicing; duplication; transmembrane protein
 F:306-329/Region: alternatively spliced segment i (exon 4) #status experimental
 F:330-350/Region: alternatively spliced segment a #status experimental
 F:538-545/Region: alternatively spliced segment b (exon 9) #status experimental
 F:874-886/Region: alternatively spliced segment e (exon 12) #status experimental
 F:887-896/Region: alternatively spliced segment f (exon 13) #status experimental
 F:958-983/Region: alternatively spliced segment h (exon 14) #status experimental

Query Match 60.7%; Score 17; DB 2; Length 1034;
 Best Local Similarity 100.0%; Pred. No. 3e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 VIGNLVNLFALILS 26
 Db 800 VIGNLVNLFALILS 816

RESULT 19
 S72467
 sodium channel protein para-type alpha chain - German cockroach (strain CSMA) (fragment)
 C:Species: Blattella germanica (German cockroach)
 A:Variety: strain CSMA
 C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
 C:Accession: S72467; S72487
 R:MiYazaki, M.; Ohyama, K.; Dunlap, D.X.; Matsumura, F.
 Mol. Genet. 252, 61-68, 1996
 A:Title: Cloning and sequencing of the para-type sodium channel gene from susceptible submitted to the EMBL Data Library, September 1996
 A:Description: Cloning and sequencing of the para-type sodium channel gene from susceptible
 A:Reference number: S72467
 A:Accession: S72467
 A:Molecule type: mRNA
 A:Residues: 1-1689 <MTY>
 A:Cross-references: UNIPROT:Q93135; EMBL:U71083; NID:G1633647; PIDN:AA82037.1; PID:G163
 R:MiYazaki, M.; Ohyama, K.; Dunlap, D.X.; Matsumura, F.
 Mol. Genet. 252, 61-68, 1996
 A:Title: Cloning and sequencing of the para-type sodium channel gene from susceptible at
 A:Reference number: S72487; MUID:96397510; PMID:8804404
 A:Accession: S72487
 A:Molecule type: mRNA
 A:Residues: 711-819 <MTM>
 A:Cross-references: EMBL:U71083
 C:Superfamily: sodium channel protein
 C:Keywords: duplication; sodium channel; transmembrane protein

Query Match 60.7%; Score 17; DB 2; Length 1689;
 Best Local Similarity 100.0%; Pred. No. 4.5e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 VIGNLVNLFALILS 26
 Db 781 VIGNLVNLFALILS 797

RESULT 20
 A33299
 sodium channel protein - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C:Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 21-Nov-1997
 C:Accession: A33299
 R:Loughney, K.; Kreber, R.; Ganetzky, B.
 Cell 58, 1143-1154, 1989
 A:Title: Molecular analysis of the para locus, a sodium channel gene in Drosophila.
 A:Reference number: A33299; MUID:89376565; PMID:2550145
 A:Accession: A33299
 A:Status: preliminary

A:Molecule type: mRNA
 A:Residues: 1-1820 <LOU>
 A:Cross-references: GB:M32078; GB:M24285
 C:Genetics:
 A:Gene: FlyBase:para
 A:Cross-references: FlyBase:FBgn0003036
 C:Superfamily: sodium channel protein
 C:Keywords: duplication; phosphoprotein; transmembrane protein

Query Match 60.7%; Score 17; DB 2; Length 1820;
 Best Local Similarity 100.0%; Pred. No. 4.8e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 VIGNLVNLFALILS 26
 Db 1004 VIGNLVNLFALILS 1020

RESULT 21
 T30902
 sodium channel SCAP1 alpha chain - California sea hare
 C:Species: Aplysia californica (California sea hare)
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T30902
 R:Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
 DNA Cell Biol. 16, 347-356, 1997
 A:Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
 A:Reference number: Z20929; MUID:97238630; PMID:9115644
 A:Accession: T30902
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1993 <DYE>
 A:Cross-references: UNIPROT:P90670; EMBL:U66915; NID:G1842248; PID:G1842249; PIDN:ANC474;
 C:Superfamily: sodium channel protein

Query Match 60.7%; Score 17; DB 2; Length 1993;
 Best Local Similarity 100.0%; Pred. No. 5.2e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 GNLVNLFLALISSP 28
 Db 971 GNLVNLFLALISSP 987

RESULT 22
 T43161
 sodium channel protein Tuna1 - sea squirt (Halocynthia roretzi)
 C:Species: Halocynthia roretzi
 C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T43161
 R:Okamura, Y.; Ono, F.; Okagaki, R.; Chong, J.; Mandel, G.
 Neuron 13, 937-948, 1994
 A:Title: Neural expression of a sodium channel gene requires cell-specific interactions.
 A:Reference number: Z22220; MUID:95033215; PMID:7946338
 A:Accession: T43161
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-2049 <OKA>
 A:Cross-references: UNIPROT:Q25150; EMBL:U71311; PIDN:BA04133.1
 C:Superfamily: sodium channel protein
 C:Keywords: sodium channel; transmembrane protein

Query Match 60.7%; Score 17; DB 2; Length 2049;
 Best Local Similarity 100.0%; Pred. No. 5.4e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 GNLVNLFLALISSP 28
 Db 1009 GNLVNLFLALISSP 1025

RESULT 23
 S72458

sodium channel protein para-type alpha chain - house fly (strain Cooper)
 C:Species: Musca domestica (house fly)
 A:Variety: Strain Cooper
 C>Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
 C:Accession: S72458
 R:Williamson, M.S.; Martinez-Torres, D.; Hick, C.A.; Devonshire, A.L.
 M:1. Gen. Genet. 252, 51-60, 1996
 A>Title: Identification of mutations in the housefly para-type sodium channel gene assoc
 A:Reference number: S72458; MUID:96397509; PMID:8804403
 A:Accession: S72458
 A:Molecule type: mRNA
 A:Residues: 1-2108 <NID>
 A:Cross-references: UNIPROT:Q94615; EMBL:X96668
 A:Experimental source: strain Cooper
 C:Genetics:
 A:Map position: 3
 C:Superfamily: sodium channel protein
 C:Keywords: alternative splicing; glycoprotein; phosphoprotein; sodium channel; transmem
 F:302,314,332,367,1451,1470/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:541,1208,1582/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 60.7%; Score 17; DB 2; Length 2108;
 Best Local Similarity 100.0%; Pred. No. 5.5e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 VIGNLVNLFALLLS 26
 |||||
 DB 1010 VIGNLVNLFALLLS 1026

RESULT 24
 A25019

sodium channel protein I - rat
 N:Alternate names: sodium channel protein A

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C:Accession: A25019; S40783; I84764

R:Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H

Nature 320, 188-192, 1986

A>Title: Existence of distinct sodium channel messenger RNAs in rat brain.

A:Reference number: A93377; MUID:86146901; PMID:3754035

A:Accession: A25019

A:Molecule type: mRNA

A:Residues: 1-2009 <NOD>

A:Cross-references: UNIPROT:P04774; GB:X03638; NID:G57216; PIDN:CAA27286.1; PID:G57217

A:Experimental source: brain

R:Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.

Nucleic Acids Res. 19, 5673-5679, 1991

A>Title: Developmentally regulated alternative RNA splicing of rat brain sodium channel

A:Reference number: S40782; MUID:9205114; PMID:1658739

A:Accession: S40783

A:Molecule type: DNA

A:Residues: 177-253 <SAR>

R:Noda, M.; Numa, S.

J. Recept. Res. 7, 467-497, 1987

A>Title: Structure and function of sodium channel.

A:Reference number: I50536; MUID:87311395; PMID:2442385

A:Accession: I84764

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-2009 <RES>

A:Cross-references: GB:M22253; NID:G1041088; PIDN:AAA79965.1; PID:G1041089

C:Superfamily: sodium channel protein

C:Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

Query Match 57.1%; Score 16; DB 2; Length 2009;

Best Local Similarity 100.0%; Pred. No. 4.6e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 NLVVNLFALLLSSF 28
 |||||
 DB 980 NLVVNLFALLLSSF 995

RESULT 25

JE0084

voltage-gated sodium channel alpha subunit - hydromedusa (Polyorchis penicillatus)

N:Alternate names: PpSCN 1

C:Species: Polyorchis penicillatus

C>Date: 11-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004

C:Accession: JE0084

R:Spafford, J.D.; Spencer, A.N.; Gallin, W.J.

Biochem. Biophys. Res. Commun. 244, 772-780, 1998

A>Title: A putative voltage-gated sodium channel alpha subunit (PpSCN1) from the hydrozo

A:Reference number: JE0084; MUID:98205197; PMID:9535741

A:Accession: JE0084

A:Molecule type: mRNA

A:Residues: 1-1695 <SPA>

A:Cross-references: UNIPROT:Q62604; GB:AF047380; NID:G3005563; PIDN:AAC38974.1; PID:G300

C:Superfamily: sodium channel protein

C:Keywords: glycoprotein

F:201,273,299,684,1065,1082,1089,1428/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 50.0%; Score 14; DB 2; Length 1695;

Best Local Similarity 100.0%; Pred. No. 3e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 VVNLFLALLLSSF 28
 |||||
 DB 704 VVNLFLALLLSSF 717

Search completed: January 27, 2005, 17:52:44
 Job time : 19 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 27, 2005, 17:35:20 ; Search time 92.5 Seconds
(without alignments)
174.167 Million cell updates/sec

Title: US-10-608-584-13

Perfect score: 28
Sequence: 1 CLTVFMVMVIGNLVNLFLALLLSF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	28	100.0	2	Q60464 cricetus
2	28	100.0	2	Q80464 cricetus
3	28	100.0	2	Q80464 cricetus
4	28	100.0	2	Q80464 cricetus
5	28	100.0	2	Q80464 cricetus
6	28	100.0	2	Q80464 cricetus
7	28	100.0	2	Q80464 cricetus
8	28	100.0	2	Q80464 cricetus
9	28	100.0	2	Q80464 cricetus
10	28	100.0	2	Q80464 cricetus
11	28	100.0	2	Q80464 cricetus
12	28	100.0	2	Q80464 cricetus
13	28	100.0	2	Q80464 cricetus
14	28	100.0	2	Q80464 cricetus
15	28	100.0	2	Q80464 cricetus
16	28	100.0	2	Q80464 cricetus
17	28	100.0	2	Q80464 cricetus
18	28	100.0	2	Q80464 cricetus
19	28	100.0	2	Q80464 cricetus
20	28	100.0	2	Q80464 cricetus
21	28	100.0	2	Q80464 cricetus
22	28	100.0	2	Q80464 cricetus
23	28	100.0	2	Q80464 cricetus
24	28	100.0	2	Q80464 cricetus
25	28	100.0	2	Q80464 cricetus
26	28	100.0	2	Q80464 cricetus
27	28	100.0	2	Q80464 cricetus
28	28	100.0	2	Q80464 cricetus
29	28	100.0	2	Q80464 cricetus
30	28	100.0	2	Q80464 cricetus
31	28	100.0	2	Q80464 cricetus

32	21	75.0	488	2	Q80078	Q80078 ictalurus p
33	21	75.0	588	2	Q80467	Q81967 xenopus lae
34	21	75.0	1136	2	Q80464	Q80464 sternopygus
35	21	75.0	1951	1	CIN3_RAT	P08104 rattus norv
36	21	75.0	1951	2	Q80467	Q80007 homo sapien
37	21	75.0	1962	2	Q75RX3	Q75RX3 homo sapien
38	21	75.0	1962	2	BAD12085	BAD12085 homo sapi
39	21	75.0	1966	2	Q925G6	Q925G6 rattus norv
40	21	75.0	2000	1	CIN3_HUMAN	Q9NY46 homo sapien
41	21	75.0	2013	2	Q865M3	Q865M3 canis famil
42	21	75.0	2015	2	Q86TR3	Q86TR3 homo sapien
43	21	75.0	2015	2	Q81ZC3	Q81ZC3 homo sapien
44	21	75.0	2015	2	Q96J69	Q96J69 homo sapien
45	21	75.0	2016	1	CIN5_HUMAN	Q14524 homo sapien
46	21	75.0	2016	2	Q75RYO	Q75RYO homo sapien
47	21	75.0	2016	2	BAD12084	BAD12084 homo sapi
48	21	75.0	2019	1	CIN5_RAT	P15389 rattus norv
49	21	75.0	2019	2	Q90JY9	Q90JY9 mus musculu
50	21	75.0	2022	2	Q8WMP8	Q8WMP8 bos tauru
51	20	71.4	742	2	Q90Z29	Q90Z29 sternopygus
52	20	67.9	1089	2	Q81S97	Q81S97 varroa deat
53	19	67.9	1130	2	Q9XZC1	Q9XZC1 boophilus m
54	19	67.9	2215	2	Q86D77	Q86D77 varroa deat
55	18	64.3	1784	2	Q25377	Q25377 loligo opal
56	17	60.7	47	2	Q6TFE2	Q6TFE2 anopheles s
57	17	60.7	47	2	Q6V9Y7	Q6V9Y7 anopheles c
58	17	60.7	47	2	Q6VE68	Q6VE68 anopheles c
59	17	60.7	47	2	Q6VE70	Q6VE70 anopheles c
60	17	60.7	47	2	Q7JNL8	Q7JNL8 heliothis v
61	17	60.7	47	2	AAR32092	AAR32092 anopheles
62	17	60.7	47	2	AAR32093	AAR32093 anopheles
63	17	60.7	47	2	AAR32094	AAR32094 anopheles
64	17	60.7	47	2	AAR32095	AAR32095 anopheles
65	17	60.7	47	2	AAR32095	AAR32095 anopheles
66	17	60.7	47	2	AAR32095	AAR32095 anopheles
67	17	60.7	124	2	Q86LC6	Q86LC6 melligethes
68	17	60.7	130	2	Q8MU84	Q8MU84 aedes aegypt
69	17	60.7	132	2	Q8IT45	Q8IT45 pediculus h
70	17	60.7	132	2	Q8IT46	Q8IT46 pediculus h
71	17	60.7	136	2	Q45207	Q45207 anopheles g
72	17	60.7	140	2	Q8KBA2	Q8KBA2 ctenocephal
73	17	60.7	140	2	Q95VK8	Q95VK8 aphid gossy
74	17	60.7	140	2	Q95VK9	Q95VK9 aphid gossy
75	17	60.7	140	2	CAC79235	CAC79235 franklini
76	17	60.7	140	2	CAC79236	CAC79236 franklini
77	17	60.7	142	2	Q97167	Q97167 culex pipie
78	17	60.7	162	2	Q710W1	Q710W1 franklini
79	17	60.7	162	2	CAC79234	CAC79234 franklini
80	17	60.7	162	2	CAC79235	CAC79235 franklini
81	17	60.7	162	2	CAC79236	CAC79236 franklini
82	17	60.7	220	2	Q95VPA	Q95VPA aphid gossy
83	17	60.7	316	2	Q18460	Q18460 haematobia
84	17	60.7	329	2	Q18461	Q18461 haematobia
85	17	60.7	335	2	Q7JP67	Q7JP67 dirosophila
86	17	60.7	340	2	Q7JP68	Q7JP68 dirosophila
87	17	60.7	348	2	Q24726	Q24726 dirosophila
88	17	60.7	508	2	Q800U2	Q800U2 ictalurus p
89	17	60.7	576	2	Q6DLU1	Q6DLU1 aedes aegypt
90	17	60.7	603	2	Q6DLT6	Q6DLT6 aedes albop
91	17	60.7	626	2	Q6DLT5	Q6DLT5 aedes albop
92	17	60.7	660	2	Q24717	Q24717 dirosophila
93	17	60.7	689	2	Q24715	Q24715 dirosophila
94	17	60.7	693	2	Q24712	Q24712 dirosophila
95	17	60.7	701	2	Q24713	Q24713 dirosophila
96	17	60.7	704	2	Q24716	Q24716 dirosophila
97	17	60.7	706	2	Q24711	Q24711 dirosophila
98	17	60.7	714	2	Q24714	Q24714 dirosophila
99	17	60.7	1087	2	Q9XYM6	Q9XYM6 leptinotars
100	17	60.7	1347	2	Q7PMT4	Q7PMT4 anopheles g

ALIGNMENTS

```

RESULT 1
Q0464 ID 060464 PRELIMINARY; PRT; 200 AA.
AC 060464;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Sodium channel alpha subunit (Fragment).
GN Name=choi;
OS Cricetus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OC NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93235989; PubMed=7682773;
RA Lalik P.H., Krafte D.S., Ciccarelli R.B.;
RT "Characterization of endogenous Sodium channel gene expressed in
RL Am. J. Physiol. 264:R03-R09(1993).
DR EMBL: M87541; AAA36979.1; -.
DR PIR: I48108; I48108.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005216; P:Ion channel activity; IEA.
DR GO: GO:0006811; P:Ion transport; IEA.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR010526; Na_trans_assoc.
DR Pfam: PF06512; Ion_trans_1.
DR Pfam: PF06512; Na_trans_assoc; 1.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW NON_TER 200
FT SEQUENCE 200 AA; 22676 MW; A09791608E43458 CRC64;
SQ

Query Match 100.0%; Score 28; DB 2; Length 200;
Best Local Similarity 100.0%; Pred. No. 3.9e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVEFMVWVIGNLVVLNLFLLALLSSF 28
Db 45 CLTVEFMVWVIGNLVVLNLFLLALLSSF 72

RESULT 2
Q8UV2 PRELIMINARY; PRT; 276 AA.
ID Q8UV2;
AC Q8UV2;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Putative voltage-activated sodium channel alpha subunit
DE (Fragment).
GN Name=scn4a;
OS Pagophantia bernacchi (Emerald rockcod) (Trematomus bernacchi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notocheniidae; Notocheniidae; Trematomus.
OC NCBI_TaxID=40690;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Skeletal muscle;
RA Moran O., Elia L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF465250; AAL6997.1; -.
DR GO: GO:0005216; P:Ion channel activity; IEA.
DR InterPro: IPR010526; Na_trans_assoc.
DR Pfam: PF06512; Na_trans_assoc; 1.
DR Ion channel.
KW NON_TER 1
FT NON_TER 276 276

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SQ SEQUENCE 276 AA; 30906 MW; 5660535780CA79B3 CRC64;
Query Match 100.0%; Score 28; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 5e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVEFMVWVIGNLVVLNLFLLALLSSF 28
Db 15 CLTVEFMVWVIGNLVVLNLFLLALLSSF 42

RESULT 3
Q80U0 PRELIMINARY; PRT; 500 AA.
ID Q80U0;
AC Q80U0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Sodium channel 5 (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OC NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu Y., Lopreato G.F., Zakon H.H.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY204536; AAO60424.1; -.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005261; P:cation channel activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR InterPro: IPR001682; Ca/Na_pore.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR005820; M_channel_1lg.
DR InterPro: IPR010526; Na_trans_assoc.
DR Pfam: PF00520; Ion_trans_1.
DR Pfam: PF06512; Na_trans_assoc; 1.
DR Ion transport; Ionic channel; Transmembrane; Transport.
KW NON_TER 1
FT NON_TER 500
SQ SEQUENCE 500 AA; 56868 MW; C7DE33040416FE3F CRC64;

Query Match 100.0%; Score 28; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 8.1e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVEFMVWVIGNLVVLNLFLLALLSSF 28
Db 6 CLTVEFMVWVIGNLVVLNLFLLALLSSF 33

RESULT 4
Q8IU6 PRELIMINARY; PRT; 1981 AA.
ID Q8IU6;
AC Q8IU6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Voltage-gated sodium channel alpha 1 subunit.
GN Name=SCN1A;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Normal brain;
RA Ouchida M., Ohmori I.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL: AB098335; BAC45228.1; -.

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DR HSPB, P04775; 1BY.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; F:cation transport; IEA.
DR GO; GO:0006814; F:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_Regiion.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR001696; Na_channel1.
DR InterPro; IPR008051; Na_channel11.
DR InterPro; IPR010526; Na_trans_assoc.
DR InterPro; IPR000100; Ribonuclease_P.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF00612; IQ_1.
DR Pfam; PF06512; Na_trans_assoc_1.
DR PRINTS; PRO0170; NACHANNEL.
DR PRINTS; PRO1664; NACHANNEL1.
DR SMART; SM00015; IQ_1.
DR PROSITE; PS00648; RIBONUCLEASE_P; UNKNOWN1.
DR Ion transport; Ionic channel; Sodium channel; Transmembrane;
DR Transport; Voltage-gated channel.
DR SEQUENCE 1981 AA; 226201 MW; B1D6946D6491B7AD CRC64;

Query March 100.0%; Score 28; DB 2; Length 1981;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CLTVFMVMVIGNLVNLFLALLLSF 28
Db 940 CLTVFMVMVIGNLVNLFLALLLSF 967

RESULT 5
CIN2 HUMAN STANDARD; PRT; 2005 AA.
AC Q99250; Q14472; Q9BZC9; Q9BZD0;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
DE subunit) (HBC II).
GN Name=SCN2A; Synonyms=SCN2A2, NAC2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA MEDLINE=92390418; PubMed=1325650;
RA Ahmed C.M., Ware D.H., Lee S.C., Paten C.D., Ferrer-Montiel A.V.,
RA Schindler A.F., McPherson J.D., Wagner-McPherson C.B., Wasmuth J.J.,
RA Evans G.A., Montiel M.;
RT "Primary structure, chromosomal localization, and functional
RT expression of a voltage-gated sodium channel from human brain.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:8220-8224(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA Kasai N., Fukushima K., Ueki Y., Praad S., Nosakowski J.,
RA Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
RT at the DPA16 locus.";
RT Gene 264:113-122(2001).
RN [3]
RP SEQUENCE OF 1-89 FROM N.A.
RA Lu C.-M., Eicheleberger J.S., Beckman M.L., Schade S.D., Brown G.B.;
RT "Isolation of the 5'-flanking region for human brain sodium channel

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RT subtype II alpha-Subunit (SCN2A).";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1702-2005 FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=92275082; PubMed=1317301;
RA Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT "Differential expression of two sodium channel subtypes in human
RT brain.";
RT FEBS Lett. 303:53-56(1992).
RN [5]
RP SEQUENCE OF 1702-1772 FROM N.A.
RX MEDLINE=91110524; PubMed=1846440;
RA Han J., Lu C.-M., Brown G.B., Rado T.A.;
RT "Direct amplification of a single dissected chromosomal segment by
RT polymerase chain reaction: a human brain sodium channel gene is on
RT chromosome 2q22-q23.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC of excitable membranes. Assuming opened or closed conformations in
CC response to the voltage difference across the membrane, the
CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC 3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Adult, 6A;
CC IsoId=Q99250-1; Sequence=Displayed;
CC Name=2; Synonyms=Neonatal, 6N;
CC IsoId=Q99250-2; Sequence=VSP_001032;
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M94055; AAA18895.1; -
CC EMBL; AF059683; AAC14574.1; -
CC EMBL; AF327246; AAG53413.1; -
CC EMBL; AF327226; AAG53413.1; JOINED.
CC EMBL; AF327227; AAG53413.1; JOINED.
CC EMBL; AF327228; AAG53413.1; JOINED.
CC EMBL; AF327229; AAG53413.1; JOINED.
CC EMBL; AF327230; AAG53413.1; JOINED.
CC EMBL; AF327231; AAG53413.1; JOINED.
CC EMBL; AF327232; AAG53413.1; JOINED.
CC EMBL; AF327233; AAG53413.1; JOINED.
CC EMBL; AF327234; AAG53413.1; JOINED.
CC EMBL; AF327235; AAG53413.1; JOINED.
CC EMBL; AF327236; AAG53413.1; JOINED.
CC EMBL; AF327237; AAG53413.1; JOINED.
CC EMBL; AF327238; AAG53413.1; JOINED.
CC EMBL; AF327239; AAG53413.1; JOINED.
CC EMBL; AF327240; AAG53413.1; JOINED.
CC EMBL; AF327241; AAG53413.1; JOINED.
CC EMBL; AF327242; AAG53413.1; JOINED.
CC EMBL; AF327243; AAG53413.1; JOINED.
CC EMBL; AF327244; AAG53413.1; JOINED.
CC EMBL; AF327245; AAG53413.1; JOINED.
CC EMBL; AF327246; AAG53412.1; -
CC EMBL; AF327226; AAG53412.1; JOINED.

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DR EMBL; AF327227; AAG53412.1; JOINED.
 DR EMBL; AF327228; AAG53412.1; JOINED.
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 DR EMBL; AF327230; AAG53412.1; JOINED.
 DR EMBL; AF327231; AAG53412.1; JOINED.
 DR EMBL; AF327232; AAG53412.1; JOINED.
 DR EMBL; AF327233; AAG53412.1; JOINED.
 DR EMBL; AF327234; AAG53412.1; JOINED.
 DR EMBL; AF327235; AAG53412.1; JOINED.
 DR EMBL; AF327236; AAG53412.1; JOINED.
 DR EMBL; AF327237; AAG53412.1; JOINED.
 DR EMBL; AF327238; AAG53412.1; JOINED.
 DR EMBL; AF327239; AAG53412.1; JOINED.
 DR EMBL; AF327240; AAG53412.1; JOINED.
 DR EMBL; AF327241; AAG53412.1; JOINED.
 DR EMBL; AF327242; AAG53412.1; JOINED.
 DR EMBL; AF327243; AAG53412.1; JOINED.
 DR EMBL; AF327244; AAG53412.1; JOINED.
 DR EMBL; AF327245; AAG53412.1; JOINED.
 DR EMBL; X65361; CA46438.1; ALT_SEQ.
 DR EMBL; M91804; -; NOT_ANNOTATED_CDS.
 DR HSSP; P04775; 1BYJ.
 DR Genew; HGNC:10588; SCN2A2.
 DR MIM; 601219; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
 DR GO; GO:0006814; P:sodium ion transport; TAS.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_Tegion.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans_4.
 DR Pfam; PF06512; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR PROSITE; PS50096; IQ_1.
 KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
 KW Multigene family; Repeat; Sodium channel; Transmembrane;
 KW Voltage-gated channel.
 FT REPEAT 111 456 I.
 FT REPEAT 741 1013 II.
 FT REPEAT 1190 1504 III.
 FT REPEAT 1513 1811 IV.
 FT TRANSMEM 125 148 S1 of repeat I.
 FT TRANSMEM 157 176 S2 of repeat I.
 FT TRANSMEM 190 208 S3 of repeat I.
 FT TRANSMEM 215 234 S4 of repeat I.
 FT TRANSMEM 251 274 S5 of repeat I.
 FT TRANSMEM 402 427 S6 of repeat I.
 FT TRANSMEM 754 778 S1 of repeat II.
 FT TRANSMEM 790 813 S2 of repeat II.
 FT TRANSMEM 822 841 S3 of repeat II.
 FT TRANSMEM 848 867 S4 of repeat II.
 FT TRANSMEM 884 904 S5 of repeat II.
 FT TRANSMEM 958 983 S6 of repeat II.
 FT TRANSMEM 1204 1227 S1 of repeat III.
 FT TRANSMEM 1241 1266 S2 of repeat III.
 FT TRANSMEM 1273 1294 S3 of repeat III.
 FT TRANSMEM 1299 1320 S4 of repeat III.
 FT TRANSMEM 1340 1367 S5 of repeat III.
 FT TRANSMEM 1447 1473 S6 of repeat III.
 FT TRANSMEM 1527 1550 S1 of repeat IV.
 FT TRANSMEM 1562 1585 S2 of repeat IV.
 FT TRANSMEM 1592 1615 S3 of repeat IV.
 FT TRANSMEM 1626 1647 S4 of repeat IV.
 FT TRANSMEM 1653 1685 S5 of repeat IV.
 FT TRANSMEM 1752 1776 S6 of repeat IV.
 FT DOMAIN 1905 1934 IQ.
 FT CARBOHYD 212 212 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 285 285 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 291 291 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 297 297 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 303 303 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 308 308 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 340 340 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 604 604 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 624 624 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 883 883 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1055 1055 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1072 1072 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1136 1136 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1368 1368 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1382 1382 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1393 1393 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1778 1778 N-linked (GlcNAc...) (Potential).
 FT VANSPLIC 209 209 D -> N (in isoform 2).
 FT CONFLICT 524 524 R -> L (in Ref. 1).
 Query March 100.0%; Score 28; DB 1; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 2.5e-17;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CLTVFMVWVIGNLVNLFLALLSSSF 28
 DB 959 CLTVFMVWVIGNLVNLFLALLSSSF 986
 ID C1N2 RAT STANDARD; PRT; 2005 AA.
 AC P04775;
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 13-AUG-1987 (Rel. 45, Last annotation update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DS Sodium channel protein type II alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha subunit).
 DE subunit).
 GN Name=Scn2a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86146901; Pubmed=3754035;
 RX Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kuraaki M., Takahashi H., Numa S.;
 RT "Existence of distinct sodium channel messenger RNAs in rat brain";
 RL Nature 320:188-192(1986).
 CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient.
 CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-3 smaller ones. This sequence represents a large polypeptide.
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.
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or send an email to license@sb-sib.ch.

CC EMBL; X03639; CAA27287.1; -.
 DR PDB; 1BY; NMR: A:1474-1526.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrypL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans_4.
 DR Pfam; PF00612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc_1.
 DR PRINTS; PR00170; NACHANNEL.
 DR PROSITE; PS50096; IQ_1.
 DR 3D-structure; Glycoprotein; Ion transport; Ionic channel;
 KM Multigene family; Repeat; Sodium channel; Transmembrane;
 KM Voltage-gated channel.
 FT REPEAT 111 456 I.
 FT REPEAT 741 1013 II.
 FT REPEAT 1190 1504 III.
 FT REPEAT 1513 1811 IV.
 FT TRANSMEM 125 148 S1 of repeat I.
 FT TRANSMEM 157 176 S2 of repeat I.
 FT TRANSMEM 190 208 S3 of repeat I.
 FT TRANSMEM 215 234 S4 of repeat I.
 FT TRANSMEM 251 274 S5 of repeat I.
 FT TRANSMEM 402 427 S6 of repeat I.
 FT TRANSMEM 754 778 S1 of repeat II.
 FT TRANSMEM 790 813 S2 of repeat II.
 FT TRANSMEM 822 841 S3 of repeat II.
 FT TRANSMEM 848 867 S4 of repeat II.
 FT TRANSMEM 884 904 S5 of repeat II.
 FT TRANSMEM 958 983 S6 of repeat II.
 FT TRANSMEM 1204 1227 S1 of repeat III.
 FT TRANSMEM 1241 1266 S2 of repeat III.
 FT TRANSMEM 1273 1294 S3 of repeat III.
 FT TRANSMEM 1299 1320 S4 of repeat III.
 FT TRANSMEM 1340 1367 S5 of repeat III.
 FT TRANSMEM 1447 1473 S6 of repeat III.
 FT TRANSMEM 1527 1550 S1 of repeat IV.
 FT TRANSMEM 1562 1585 S2 of repeat IV.
 FT TRANSMEM 1592 1615 S3 of repeat IV.
 FT TRANSMEM 1626 1647 S4 of repeat IV.
 FT TRANSMEM 1663 1685 S5 of repeat IV.
 FT TRANSMEM 1752 1776 S6 of repeat IV.
 FT DOMAIN 1905 1934 IQ.
 FT CARBOHYD 212 212 N-linked (GlcNAc...)
 FT CARBOHYD 285 285 N-linked (GlcNAc...)
 FT CARBOHYD 291 291 N-linked (GlcNAc...)
 FT CARBOHYD 297 297 N-linked (GlcNAc...)
 FT CARBOHYD 303 303 N-linked (GlcNAc...)
 FT CARBOHYD 308 308 N-linked (GlcNAc...)
 FT CARBOHYD 340 340 N-linked (GlcNAc...)
 FT CARBOHYD 604 604 N-linked (GlcNAc...)
 FT CARBOHYD 624 624 N-linked (GlcNAc...)
 FT CARBOHYD 883 883 N-linked (GlcNAc...)
 FT CARBOHYD 1055 1055 N-linked (GlcNAc...)
 FT CARBOHYD 1072 1072 N-linked (GlcNAc...)
 FT CARBOHYD 1136 1136 N-linked (GlcNAc...)
 FT CARBOHYD 1368 1368 N-linked (GlcNAc...)
 FT CARBOHYD 1382 1382 N-linked (GlcNAc...)
 FT CARBOHYD 1393 1393 N-linked (GlcNAc...)
 SQ SEQUENCE 2005 AA; 227872 MW; 861BE583D79F8324 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 2.Se-17;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMVMVIGNLVNLFLALLLSF 28
 Db 959 CLTVFMVMVIGNLVNLFLALLLSF 986

RESULT 7

Q9YGN7

ID Q9YGN7 PRELIMINARY; PRT; 2007 AA.

AC Q9YGN7 01-MAY-1999 (TRENBLrel. 10, Created)

DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Voltage-dependent sodium channel.

OS Cynops pyrrhogaster (Japanese common newt).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.

OX NCBI_TaxId=8330;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Retina;

RA Hirota K., Kaneko Y., Matsumoto G., Hanyu Y.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the sodium channel family.

DR EMBL; AF133593; AAD17315.1; -.

DR HSSP; P04775; 1BY1.

DR GO; GO:0016021; C:Integral to membrane; IEA.

DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.

DR GO; GO:0005261; F:cation channel activity; IEA.

DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.

DR GO; GO:0006812; F:cation transport; IEA.

DR GO; GO:0006814; P:sodium ion transport; IEA.

DR InterPro; IPR001682; Ca/Na_pore.

DR InterPro; IPR002111; Cat_channel_TrypL.

DR InterPro; IPR005821; Ion_trans.

DR InterPro; IPR000048; IQ_region.

DR InterPro; IPR005820; M-channel_nlg.

DR InterPro; IPR001696; Na_channel.

DR Pfam; PF00520; Ion_trans_4.

DR Pfam; PF06512; IQ_1.

DR PRINTS; PR00170; NACHANNEL.

DR SMART; SM00015; IQ_1.

KM Ion transport; Ionic channel; Sodium channel; Transmembrane;

KM Transport; Voltage-gated channel.

SQ SEQUENCE 2007 AA; 228398 MW; 013B9B9C9C294C9 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 2.Se-17;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMVMVIGNLVNLFLALLLSF 28
 Db 957 CLTVFMVMVIGNLVNLFLALLLSF 984

RESULT 8

ID CINI_HUMAN STANDARD; PRT; 2009 AA.

AC P35498; Q16172; Q96LA3; Q9C008;

DT 01-JUN-1994 (Rel. 29, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Sodium channel protein type I alpha subunit (Voltage-gated sodium

DE channel alpha subunit Nav1.1) (Sodium channel protein, Brain I alpha

DE subunit).

DE Name=SCN1A; Synonym=SCN1; NAcl1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GEF5+2 MET-875 AND

RP HIS-1648.

RX MEDLINE=20206553; PubMed=10742094;

RA Escayg A., MacDonald B.T., Weisler M.H., Baulac S., Huberfeld G.,
 RA An-Goufinkel I., Brice A., Leclercq E., Moulard B., Chaigne D.,
 RA Buresi C., Mafafosse A.;
 RT "Mutations of SCN1A, encoding a neuronal sodium channel, in two
 RT families with GERS+2."; *Nat. Genet.* 24:343-345(2000).
 RL (12)
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RA Jeong S.-Y., Goto J., Kanazawa I.;
 RT "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
 RT SCN1A."; *Submitted (JAN-2000) to the EMBL/genbank/DBJ databases.*
 RL (13)
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RA Sugawara T., Mazaki E.M., Yamakawa K.;
 RT "Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
 RT mRNA."; *Submitted (JUL-2001) to the EMBL/genbank/DBJ databases.*
 RL (14)
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT THR-1067.
 RA Ouchida M., Ohmori I.;
 RT "Isoforms of human sodium channel SCN1A gene."; *Submitted (OCT-2002) to the EMBL/genbank/DBJ databases.*
 RN (15)
 RN SEQUENCE OF 1335-1428 FROM N.A.
 RP MEDLINE=94340991; PubMed=8062593;
 RA Malo M.S., Blanchard B.J., Andresen J.M., Srivastava K., Chen X.N.,
 RA Li X., Jabs E.W., Korenberg J.R., Ingiram V.M.;
 RT "Localization of a putative human brain sodium channel gene (SCN1A) to
 RT chromosome band 2q24."; *Cytogenet. Cell Genet.* 67:178-186(1994).
 RL (16)
 RN SEQUENCE OF 1518-1940 FROM N.A.
 RP TISSUE=Brain;
 RA MEDLINE=92275082; PubMed=1117301;
 RC Lu C.-W., Han J., Rado T.A., Brown G.B.;
 RT "Differential expression of two sodium channel subtypes in human
 RT brain."; *FEBS Lett.* 303:53-58(1992).
 RL (17)
 RN VARIANTS GERS+2 VAL-188, LEU-1353 AND MET-1656.
 RP MEDLINE=21152274; PubMed=11254444;
 RA Wallace R.H., Scheffer I.E., Barnett S., Richards M., Dibbens L.,
 RA Desai R.R., Lerman-Sagie T., Lev D., Mazarib A., Brand N.,
 RA Ben-Zeev B., Golthman I., Singh R., Kremidiortis G., Gardner A.,
 RA Suberland G.R., George A.L., Jr., Mulley J.C., Berkovic S.F.;
 RT "Neuronal sodium-channel alpha1-subunit mutations in generalized
 RT epilepsy with febrile seizures plus."; *Am. J. Hum. Genet.* 68:859-865(2001).
 RL (18)
 RN VARIANTS GERS+2 ARG-1204,
 RP MEDLINE=21152275; PubMed=11254445;
 RA Escayg A., Hells A., MacDonald B.T., Haug K., Sander T., Weisler M.H.;
 RT "A novel SCN1A mutation associated with generalized epilepsy with
 RT febrile seizures plus -- and prevalence of variants in patients with
 RT epilepsy."; *Am. J. Hum. Genet.* 68:866-873(2001).
 RL (19)
 RN VARIANT SMEI-PHE-986.
 RP MEDLINE=21257503; PubMed=11359211;
 RA Ciles L., Del-Favero J., Culemans B., Lagae L., Van Broeckhoven C.,
 RA De Jonghe P.;
 RT "De novo mutations in the sodium-channel gene SCN1A cause severe
 RT myoclonic epilepsy of infancy."; *Am. J. Hum. Genet.* 68:1327-1332(2001).
 RL (10)
 RN VARIANT GERS+2 THR-1270.
 RP MEDLINE=21630138; PubMed=11756608;
 RA Abou-Khalil B., Ge O., Desai R., Ryther R., Bazzyk A., Bailey R.,
 RA Haines J.L., Sutcliffe J.S., George A.L., Jr.;
 RT "Partial and generalized epilepsy with febrile seizures plus and a
 RT novel SCN1A mutation.";

RL Neurology 57:2265-2272(2001).
 CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
 CC of excitable membranes. Assuming opened or closed conformations in
 CC response to the voltage difference across the membrane, the
 CC protein forms a sodium-selective channel through which Na(+) ions
 CC may pass in accordance with their electrochemical gradient.
 CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
 CC 3 smaller ones. This sequence represents a large polypeptide.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P35498-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P35498-2; Sequence=VSP_001031;
 CC Note=No experimental confirmation available;
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- DISEASE: Defects in SCN1A are the cause of generalized epilepsy
 CC with febrile seizures plus type 2 (GERS+2) [MIM:604233]. This
 CC autosomal dominant disorder is characterized by febrile seizures
 CC in children and afebrile seizures in adults. Penetrance is
 CC incomplete and a large intrafamilial variability of the phenotype
 CC is observed.
 CC -1- DISEASE: Defects in SCN1A are a cause of severe myoclonic epilepsy
 CC in infancy (SMEI) [MIM:607208], a severe form of generalized
 CC epilepsy with febrile seizures. SMEI is a rare disorder
 CC characterized by normal development before onset, seizures
 CC beginning in the first year of life in the form of generalized or
 CC unilateral febrile clonic seizures, secondary appearance of
 CC myoclonic seizures, and occasionally partial seizures. It is
 CC associated with ataxia, slowed psychomotor development, and mental
 CC decline.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC -----
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 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF225985; AAK00217.1; -;
 CC EMBL; AY043484; AAK95360.1; -;
 CC EMBL; AB093548; BAC21101.1; -;
 CC EMBL; AB093549; BAC21102.1; -;
 CC EMBL; S71446; AAB31605.1; -;
 CC EMBL; X65362; CAA46439.1; -;
 CC EMBL; M91803; -; NOT_ANNOTATED_CDS.
 CC PIR; I52964; I52964.
 CC PIR; S29184; S29184.
 CC HSSP; P04775; 1BYT.
 CC Genew; HGNC:10585; SCN1A.
 CC MIM; 182389; -;
 CC MIM; 604233; -;
 CC MIM; 607208; -;
 CC GO; GO:0016021; C:integral to membrane; NAS.
 CC GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
 CC GO; GO:0006814; P:sodium ion transport; NAS.
 CC InterPro; IPR001682; Ca/Na_pore.
 CC InterPro; IPR002111; Cat_channel_TrypL.
 CC InterPro; IPR005821; Ion_trans.
 CC InterPro; IPR000048; IQ_region.
 CC InterPro; IPR005820; M+channel_nlg.
 CC InterPro; IPR001696; Na_channel.
 CC InterPro; IPR008051; Na_channel1.
 CC InterPro; IPR010526; Na_trans_assoc.
 CC Pfam; Pf00520; Ion_trans; 4.

```

DR Pfam; PF00612; IQ; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PRO0170; NACHANNEL.
DR PRINTS; PRO1664; NACHANNEL.
DR PROSITE; PS00966; IQ; FALSE_NEG.
KW Alternative splicing; Disease mutation; Epilepsy; Glycoprotein;
KW Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat;
KW Sodium channel; Transmembrane; Voltage-gated channel.
FT REPEAT 110 454
FT REPEAT 750 1022
FT REPEAT 1200 1514
FT REPEAT 1523 1821
FT TRANSMEM 124 147
FT TRANSMEM 156 175
FT TRANSMEM 189 207
FT TRANSMEM 214 233
FT TRANSMEM 250 273
FT TRANSMEM 400 425
FT TRANSMEM 763 787
FT TRANSMEM 799 822
FT TRANSMEM 831 850
FT TRANSMEM 857 876
FT TRANSMEM 893 913
FT TRANSMEM 967 992
FT TRANSMEM 1214 1237
FT TRANSMEM 1251 1276
FT TRANSMEM 1283 1304
FT TRANSMEM 1309 1330
FT TRANSMEM 1350 1377
FT TRANSMEM 1457 1483
FT TRANSMEM 1537 1560
FT TRANSMEM 1572 1595
FT TRANSMEM 1602 1625
FT TRANSMEM 1636 1657
FT TRANSMEM 1673 1695
FT TRANSMEM 1762 1786
FT CARBOHYD 211 211

Query Match 100.0%; Score 28; DB 1; Length 2009;
Best Local Similarity 100.0%; Pred. No. 2.5e-17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CLTVFMVWVIGNLVNLFLLALLSSP 28
Db 968 CLTVFMVWVIGNLVNLFLLALLSSP 995

RESULT 9
Q08004 PRELIMINARY; PRT; 472 AA.
AC Q08004.
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Sodium channel 1 (Fragment).
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxId=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu Y., Lopreato G.F., Zakon H.H.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY204532; AA060420.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 1.

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DR Pfam; PF06512; Na_trans_assoc; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 472
SQ SEQUENCE 472 AA; 53917 MW; 3DD68F4EAB484FAB CRC64;

Query Match 89.3%; Score 25; DB 2; Length 472;
Best Local Similarity 100.0%; Pred. No. 4.8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VPMWVWVIGNLVNLFLLALLSSP 28
Db 9 VPMWVWVIGNLVNLFLLALLSSP 33

RESULT 10
Q09026 PRELIMINARY; PRT; 743 AA.
AC Q09026.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Sodium channel 5 (Fragment).
OS Sternohyus macrurus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC Sternopygidae; Sternopygus.
OX NCBI_TaxId=77841;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21310016; PubMed=11416226;
RA Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA Wilcox T.P., Zakon H.H.;
RT "Evolution and divergence of sodium channel genes in vertebrates."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR EMBL; AF378143; AAK55441.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrtL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 2.
DR Pfam; PF06512; Na_trans_assoc; 1.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 743
SQ SEQUENCE 743 AA; 84781 MW; F2429665544CABOC CRC64;

Query Match 89.3%; Score 25; DB 2; Length 743;
Best Local Similarity 100.0%; Pred. No. 7e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VPMWVWVIGNLVNLFLLALLSSP 28
Db 182 VPMWVWVIGNLVNLFLLALLSSP 206

RESULT 11
Q09028 PRELIMINARY; PRT; 751 AA.
AC Q09028.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Sodium channel 3 (Fragment).
OS Sternohyus macrurus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC Sternopygidae; Sternopygus.
OX NCBI_TaxId=77841;

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DB 803 VFMWVIGNLVNLFLALLSSP 827

RESULT 14

ID 09DF53 PRELIMINARY; PRT; 1949 AA.

AC 09DF53;

DT 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Sodium channel protein Scn8a.

GN Name=Scn8a;

OS Brachydanio rerio (Zebrafish) (Danio rerio).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Danio.

OC NCBI_TaxId=7955;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=oregon;

RL Tsai C.-W., Tseng J.-J., Horng J.-F., Wu J.-L., Tsay H.-J.;

CC Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the sodium channel family.

DR EMBL; AF297658; AAG18440.1; -.

DR HSSP; P04775; 1BYX.

DR ZFIN; ZDB-GENE-000828-1; scn8a.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.

DR GO; GO:0005261; F:cation channel activity; IEA.

DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR GO; GO:0006814; P:sodium ion transport; IEA.

DR InterPro; IPR001682; Ca/Na_pore.

DR InterPro; IPR002111; Cat_channel_TrypL.

DR InterPro; IPR005821; Ion_trans.

DR InterPro; IPR000048; IQ_region.

DR InterPro; IPR005820; M+channel_nlg.

DR InterPro; IPR001696; Na_channel.

DR InterPro; IPR008054; Na_channel18.

DR InterPro; IPR010526; Na_trans_assoc.

DR Pfam; PF00520; Ion_trans_4.

DR Pfam; PF06512; IQ_1.

DR Pfam; PF06512; Na_trans_assoc; 1.

DR PRINTS; PR00170; NACHANNEL.

DR PRINTS; PR01667; NACHANNEL8.

DR SMART; SM00015; IQ_1.

KW Ion transport; Ionic channel; Sodium channel; Transmembrane;

KW Transport; Voltage-gated channel.

SO SEQUENCE 1949 AA; 221760 MW; 6BCA69664BDC7BC3 CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1949;

Best Local Similarity 100.0%; Pred. No. 1.5e-14;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFMWVIGNLVNLFLALLSSP 28

Db 925 VFMWVIGNLVNLFLALLSSP 949

RESULT 15

ID 063541 PRELIMINARY; PRT; 1976 AA.

AC 063541;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE Sodium channel protein 6.

GN Name=SCN6;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OC NCBI_TaxId=10116;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain;

RX MEDLINE=95271284; PubMed=7751906;

RA Schaller K.L., Kizemien D.M., Yarowsky P.J., Krueger B.K.,

RA Caldwell J.H.;

RT "A novel, abundant sodium channel expressed in neurons and glia.";

RL J. Neurosci. 15:3231-3242 (1995).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- SIMILARITY: Belongs to the sodium channel family.

DR EMBL; L39018; AAC42059.1; -.

DR PIR; I56555; I56555.

DR HSSP; P04775; 1BYX.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.

DR GO; GO:0005261; F:cation channel activity; IEA.

DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.

DR GO; GO:0006814; P:sodium ion transport; IEA.

DR InterPro; IPR001682; Ca/Na_pore.

DR InterPro; IPR002111; Cat_channel_TrypL.

DR InterPro; IPR000183; Decarboxylase2.

DR InterPro; IPR005821; Ion_trans.

DR InterPro; IPR000048; IQ_region.

DR InterPro; IPR005820; M+channel_nlg.

DR InterPro; IPR001696; Na_channel18.

DR InterPro; IPR008054; Na_channel.

DR InterPro; IPR010526; Na_trans_assoc.

DR Pfam; PF00520; Ion_trans_4.

DR Pfam; PF00612; IQ_1.

DR Pfam; PF06512; Na_trans_assoc; 1.

DR PRINTS; PR00170; NACHANNEL.

DR PRINTS; PR01667; NACHANNEL8.

DR SMART; SM00015; IQ_1.

DR PROSITE; PS50096; IQ_1.

DR PROSITE; PS00878; ODR DC 2.1; UNKNOWN 1.

KW Ion transport; Ionic channel; Sodium channel; Transmembrane;

KW Transport; Voltage-gated channel.

SO SEQUENCE 1976 AA; 225227 MW; B6949327A47FA88A CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1976;

Best Local Similarity 100.0%; Pred. No. 1.5e-14;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFMWVIGNLVNLFLALLSSP 28

Db 952 VFMWVIGNLVNLFLALLSSP 976

RESULT 16

ID C1N8_MOUSE STANDARD; PRT; 1978 AA.

AC 09WTU3; Q60828; Q60858; Q62449;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Sodium channel protein type VIII alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.6).

DE channel alpha subunit Nav1.6).

GN Name=Scn8a; Synonyms=Nbnal1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxId=10090;

RN (1)

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).

RC STRAIN=C57BL/6J;

RX MEDLINE=99047535; PubMed=9828131;

RA Plummer N.W., Galt J., Jones J.M., Burgess D.L., Sprunger L.K.,

RA Kohrman D.C., Meisler M.H.;

RT "Exon organization, coding sequence, physical mapping, and polymorphic

RT intragenic markers for the human neuronal sodium channel gene SCN8A.";

RL Genomics 54:287-296 (1998).

RN (2)

RP SEQUENCE FROM N.A. (ISOFORM 2), TISSUE SPECIFICITY, AND DISEASE.
 RC STRAIN=557BL/6J; TISSUE=Brain;
 RX MEDLINE=95400328; PubMed=7670495;
 RA Burgess D.L., Kohman D.C., Galt J., Plummer N.W., Jones J.M.,
 RA Spear B., Meister M.H.;
 RT "Mutation of a new sodium channel gene, Scn8a, in the mouse mutant
 RT 'motor endplate disease'.";
 RL Nat. Genet. 10:461-465(1995).
 RN [3]
 RP SEQUENCE OF 93-205 FROM N.A., AND DISEASE.
 RC STRAIN=129/Sv; TISSUE=Brain;
 RX MEDLINE=96291923; PubMed=8663325;
 RA Kohman D.C., Harris J.B., Meister M.H.;
 RT "Mutation detection in the med and medu alleles of the sodium channel
 RT Scn8a. Unusual splicing due to a minor class AT-AC intron.";
 RL J. Biol. Chem. 271:17576-17581(1996).
 RN [4]
 RP SEQUENCE OF 1411-1686 FROM N.A.
 RA Fan Z., Kyle J.W., Makleiski J.C.;
 RT "A putative novel Na channel alpha subunit cDNA isolated from mouse
 RT NB2a neuroblastoma cells.";
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP ALTERNATIVE SPLICING (ISOFORMS 1; 4 AND 5).
 RC TISSUE=Brain, and fetal brain;
 RX MEDLINE=97442476; PubMed=9295353;
 RA Plummer N.W., McBurney M.W., Meister M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 RT two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 RN [6]
 RP VARIANT MEDJO THR-1317, AND VARIANT LEU-5.
 RC STRAIN=DBA/2MYD1;
 RX MEDLINE=96424513; PubMed=8815882;
 RA Kohman D.C., Smith M.R., Goldin A.L., Harris J., Meister M.H.;
 RT "A missense mutation in the sodium channel Scn8a is responsible for
 RT cerebellar ataxia in the mouse mutant jolting.";
 RL J. Neurosci. 16:5993-5999(1996).
 RN [7]
 RP DISEASE.
 RX MEDLINE=21423786; PubMed=11532991;
 RA De Repentigny Y., Core P.D., Pool M., Bernier G., Girard S.,
 RA Vidal S.M., Kochary R.;
 RT "Pathological and genetic analysis of the degenerating muscle (dmu)
 RT mouse: a new allele of Scn8a.";
 RL Hum. Mol. Genet. 10:1819-1827(2001).
 CC -!- FUNCTION: Mediates the voltage-dependent sodium ion permeability
 CC of excitable membranes. Assuming opened or closed conformations in
 CC response to the voltage difference across the membrane, the
 CC protein forms a sodium-selective channel through which Na(+) ions
 CC may pass in accordance with their electrochemical gradient.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=18a;
 CC IsoId=Q9WTU3-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9WTU3-2; Sequence=VSP_050594;
 CC Name=3;
 CC IsoId=Q9WTU3-3; Sequence=VSP_050595;
 CC Name=4; Synonyms=18n;
 CC IsoId=Q9WTU3-4; Sequence=VSP_050596, VSP_050597;
 CC Name=5;
 CC IsoId=Q9WTU3-5; Sequence=VSP_050598;
 CC -!- TISSUE SPECIFICITY: Expressed in brain, cerebellum and spinal
 CC cord.
 CC -!- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -!- DISEASE: Defects in Scn8a are the cause of motor endplate disease
 CC (med). Med is a recessive neuromuscular disorder that is

CC characterized by lack of signal transmission at the neuromuscular
 CC junction, excess preterminal arborization and degeneration of
 CC cerebellar Purkinje cells. It produces early onset progressive
 CC paralysis of hind limbs, severe muscle atrophy and juvenile
 CC lethality.
 CC -!- DISEASE: Defects in Scn8a are the cause of the jolting mutant
 CC (medjo), a mild form of motor endplate disease which is
 CC characterized by the absence of spontaneous, regular, simple
 CC discharges from Purkinje cells. After 3 weeks of age, jolting mice
 CC are unsteady and have wide-based gait and a rhythmic tremor of
 CC head and neck induced by attempted movement.
 CC -!- DISEASE: Defects in Scn8a are a cause of degenerating muscle
 CC (dmu). Dmu is an autosomal recessive neuromuscular disorder that
 CC is characterized by skeletal and cardiac muscle degeneration. It
 CC produces early onset progressive loss of mobility of the hind
 CC limbs and subsequent lethality in the first month of life.
 CC -!- SIMILARITY: Belongs to the sodium channel family.
 CC -!- SIMILARITY: Contains 1 IQ domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC DR EMBL, AF049617; AAD20438.1; -.
 CC DR EMBL, U26707; AAC52242.1; -.
 CC DR EMBL, U59964; AAC52708.1; -.
 CC DR EMBL, U59963; AAC52708.1; JOINED.
 CC DR EMBL, U23158; AAA65599.1; -.
 CC DR HSSP, P04775; 1BYX.
 CC DR MGD, MGI:103169; Scn8a.
 CC DR GO, GO:0005158; C:voltage-gated sodium channel complex; IC.
 CC DR GO, GO:0005248; F:voltage-gated sodium channel activity; MAS.
 CC DR GO, GO:0007628; P:adult walking behavior; IMP.
 CC DR GO, GO:0006814; P:sodium ion transport; NAS.
 CC DR InterPro: IPR001682; Ca/Na pore.
 CC DR InterPro: IPR002111; Cat_channel_TrypL.
 CC DR InterPro: IPR005821; Ion_trans.
 CC DR InterPro: IPR000048; IQ_region.
 CC DR InterPro: IPR005820; M-channel_nlg.
 CC DR InterPro: IPR001696; Na_channel_1.
 CC DR InterPro: IPR008054; Na_channel18.
 CC DR InterPro: IPR010526; Na_trans_assoc.
 CC DR Pfam, PF00520; Ion_trans, 4.
 CC DR Pfam, PF0612; IQ_1.
 CC DR Pfam, PF06512; Na_trans_assoc; 1.
 CC DR PRINTS, PR00170; NACHANNEL.
 CC DR PRINTS, PRO1667; NACHANNEL8.
 CC DR PROSITE, PS0096; IQ, 1.
 CC KM Alternative splicing; ATP-binding; Disease mutation; Glycoprotein;
 CC KM Ion transport; Ionic channel; Multigene family; Polynorphism; Repeat;
 CC KM Sodium channel; Transmembrane; Voltage-gated channel.
 CC FT REPEAT 114 442 I.
 CC FT REPEAT 733 1005 II.
 CC FT REPEAT 1178 1493 III.
 CC FT REPEAT 1502 1799 IV.
 CC FT TRANSMEM 128 151
 CC FT TRANSMEM 160 179
 CC FT TRANSMEM 193 211
 CC FT TRANSMEM 218 237
 CC FT TRANSMEM 253 277
 CC FT TRANSMEM 388 413
 CC FT TRANSMEM 746 770
 CC FT TRANSMEM 782 805
 CC FT TRANSMEM 814 833
 CC FT TRANSMEM 840 860
 CC FT TRANSMEM 876 896
 CC FT TRANSMEM 950 975
 CC FT TRANSMEM 1192 1215
 CC FT TRANSMEM 1229 1254
 CC S2 of repeat I.
 CC S2 of repeat I.
 CC S3 of repeat I.
 CC S4 of repeat I.
 CC S5 of repeat I.
 CC S6 of repeat I.
 CC S1 of repeat II.
 CC S2 of repeat II.
 CC S3 of repeat II.
 CC S4 of repeat II.
 CC S5 of repeat II.
 CC S6 of repeat II.
 CC S1 of repeat III.
 CC S2 of repeat III.

FT TRANSMEM 1261 1282 S3 of repeat III.
 FT TRANSMEM 1267 1308 S4 of repeat III.
 FT TRANSMEM 1328 1349 S5 of repeat III.
 FT TRANSMEM 1436 1462 S6 of repeat III.
 FT TRANSMEM 1516 1539 S1 of repeat IV.
 FT TRANSMEM 1551 1574 S2 of repeat IV.
 FT TRANSMEM 1581 1604 S3 of repeat IV.
 FT TRANSMEM 1615 1636 S4 of repeat IV.
 FT TRANSMEM 1652 1674 S5 of repeat IV.
 FT TRANSMEM 1740 1764 S6 of repeat IV.
 FT DOMAIN 1893 1922 IO.
 NP_BIND 891 898 ATP (Potential).
 FT CARBOHYD 215 215 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 289 289 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 295 295 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 308 308 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 326 326 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 544 544 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 640 640 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 875 875 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1045 1045 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1062 1062 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1089 1089 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1356 1356 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1370 1370 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1381 1381 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1766 1766 N-1-linked (GlcNAc. . .) (Potential).
 FT VANSPLC 428 673 Missing (in isoform 2).
 VANSPLC 664 664 /FTId=VSP_050594.
 FT VANSPLC 664 664 E -> EVKIDKATDS (in isoform 3).
 FT VANSPLC 664 664 /FTId=VSP_050595.
 FT VANSPLC 1273 1280 SLVSLIAN -> PLSISGLI (in isoform 4).

Query Match 89.3%; Score 25; DB 1; Length 1978;
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VPMWVIGNLVNLFLALLSSSF 28
 |||||
 DB 954 VPMWVIGNLVNLFLALLSSSF 978

RESULT 17
 088420 PRELIMINARY; PRT; 1978 AA.
 AC 088420:
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Voltage-gated sodium channel rRNA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Dorsal root ganglia;
 RX MEDLINE=96264329; PubMed=9603190;
 RA Dietrich P.S., McGivern J.G., Delgado S.G., Koch B.D., Eglen R.M.,
 RA Hunter J.C., Sangameswaran L.;
 RT "Functional analysis of a voltage-gated sodium channel and its splice
 RT variant from rat dorsal root ganglia.";
 RL J. Neurochem. 70:2262-2272(1998).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; AF049239; AAC26014.1; -.
 DR HSSP; P04775; 1BYX.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.

DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TpL.
 DR InterPro; IPR000183; Decarboxylase2.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IO_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR008054; Na_channel8.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PR00520; Ion_trans; 4.
 DR Pfam; PR00612; IO_1.
 DR Pfam; PR06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR PRINTS; PR01667; NACHANNEL8.
 DR SMART; SM00015; IO; 1.
 DR PROSITE; PS00096; IO; 1.
 DR PROSITE; PS00878; ODR_DC_2.1; UNKNOWN_1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 1978 AA; 225157 MW; 9160843C5935B88B CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1978;
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VPMWVIGNLVNLFLALLSSSF 28
 |||||
 DB 954 VPMWVIGNLVNLFLALLSSSF 978

RESULT 18
 CINH HUMAN STANDARD; PRT; 1980 AA.
 ID CINH HUMAN
 AC 09U0D0; O95788; G9NYX2; G9UPB2;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel protein type VIII alpha subunit (Voltage-gated sodium
 DE channel alpha subunit Nav1.6).
 GN Name=SCN8A;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 4).
 RC TISSUE=Brain, and Fetal brain;
 RX MEDLINE=97442476; PubMed=9295353;
 RA Plummer N.W., McBurney M.W., Weisler M.H.;
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
 RT two-domain protein in fetal brain and non-neuronal cells.";
 RL J. Biol. Chem. 272:24008-24015(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RX MEDLINE=99047535; PubMed=9828131;
 RA Plummer N.W., Galt J., Jones J.M., Burgess D.L., Sprunger L.K.,
 RA Kohman D.C., Weisler M.H.;
 RT "Exon organization, coding sequence, physical mapping, and polymorphic
 RT intragenic markers for the human neuronal sodium channel gene SCN8A.";
 RL Genomics 54:287-296(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Lin C., Numakura C., Kiyoshi H.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Jeong S.-Y., Goto J., Kanazawa I.;
 RT "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
 RT SCN8A.";
 CC -1- FUNCTION: Mediates the EMBL/GenBank/DBJ databases.
 CC of excitable membranes. Assuming opened or closed conformations in
 CC response to the voltage difference across the membrane, the

CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9UQD0-1; Sequence=Displayed;
CC Name=2; Synonyms=5A;
CC IsoId=Q9UQD0-2; Sequence=VSP_050589, VSP_050590;
CC Name=3;
CC IsoId=Q9UQD0-3; Sequence=VSP_050591;
CC Name=4; Synonyms=18N;
CC IsoId=Q9UQD0-4; Sequence=VSP_050592, VSP_050593;
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF050736; AAD15789.1; -.
DR EMBL; AF050711; AAD15789.1; JOINED.
DR EMBL; AF050712; AAD15789.1; JOINED.
DR EMBL; AF050713; AAD15789.1; JOINED.
DR EMBL; AF050714; AAD15789.1; JOINED.
DR EMBL; AF050715; AAD15789.1; JOINED.
DR EMBL; AF050716; AAD15789.1; JOINED.
DR EMBL; AF050717; AAD15789.1; JOINED.
DR EMBL; AF050718; AAD15789.1; JOINED.
DR EMBL; AF050719; AAD15789.1; JOINED.
DR EMBL; AF050720; AAD15789.1; JOINED.
DR EMBL; AF050721; AAD15789.1; JOINED.
DR EMBL; AF050722; AAD15789.1; JOINED.
DR EMBL; AF050723; AAD15789.1; JOINED.
DR EMBL; AF050724; AAD15789.1; JOINED.
DR EMBL; AF050725; AAD15789.1; JOINED.
DR EMBL; AF050726; AAD15789.1; JOINED.
DR EMBL; AF050727; AAD15789.1; JOINED.
DR EMBL; AF050728; AAD15789.1; JOINED.
DR EMBL; AF050729; AAD15789.1; JOINED.
DR EMBL; AF050730; AAD15789.1; JOINED.
DR EMBL; AF050731; AAD15789.1; JOINED.
DR EMBL; AF050732; AAD15789.1; JOINED.
DR EMBL; AF050733; AAD15789.1; JOINED.
DR EMBL; AF050734; AAD15789.1; JOINED.
DR EMBL; AF050735; AAD15789.1; JOINED.
DR EMBL; AF049618; AAD20439.1; -.
DR EMBL; AB027567; BAA78033.1; -.
DR EMBL; AF225988; AAF35390.1; -.
DR HSSP; P04775; 1BYX.
DR Genew; HGNC:10596; SCN8A.
DR MIM; 600702; -.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IC.
DR GO; GO:0005248; C:voltage-gated sodium channel activity; NAS.
DR GO; GO:0006814; P:sodium ion transport; NAS.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR008054; Na_channel18.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.

DR Pfam; PF00612; IQ; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PRINTS; PR01657; NACHANNEL8.
DR PROSITE; PS50096; IQ; 1.
KW Alternative splicing; ATP-binding; Glycoprotein; Ion transport;
KW Ionic channel; Multigene family; Repeat; Sodium channel;
KW Transmembrane; Voltage-gated channel.
FT REPEAT 114 442
FT Name=3 I.
FT REPEAT 735 1007 II.
FT REPEAT 1180 1495 III.
FT REPEAT 1504 1801 IV.
FT TRANSMEM 128 151 S1 of repeat I.
FT TRANSMEM 160 179 S2 of repeat I.
FT TRANSMEM 193 211 S3 of repeat I.
FT TRANSMEM 218 237 S4 of repeat I.
FT TRANSMEM 253 277 S5 of repeat I.
FT TRANSMEM 388 413 S6 of repeat I.
FT TRANSMEM 748 772 S1 of repeat II.
FT TRANSMEM 784 807 S2 of repeat II.
FT TRANSMEM 816 835 S3 of repeat II.
FT TRANSMEM 842 862 S4 of repeat II.
FT TRANSMEM 878 898 S5 of repeat II.
FT TRANSMEM 952 977 S6 of repeat II.
FT TRANSMEM 1194 1217 S1 of repeat III.
FT TRANSMEM 1231 1256 S2 of repeat III.
FT TRANSMEM 1263 1284 S3 of repeat III.
FT TRANSMEM 1289 1310 S4 of repeat III.
FT TRANSMEM 1330 1351 S5 of repeat III.
FT TRANSMEM 1438 1464 S6 of repeat III.
FT TRANSMEM 1518 1541 S1 of repeat IV.
FT TRANSMEM 1553 1576 S2 of repeat IV.
FT TRANSMEM 1583 1606 S3 of repeat IV.
FT TRANSMEM 1617 1638 S4 of repeat IV.
FT TRANSMEM 1654 1676 S5 of repeat IV.
FT TRANSMEM 1742 1766 S6 of repeat IV.
FT DOMAIN 1895 1924 IQ.
FT NP BIND 893 900 ATP (Potential).
FT CARBOHYD 215 215 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 289 289 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 295 295 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 308 308 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 326 326 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 544 544 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 640 640 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 877 877 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 1047 1047 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 1064 1064 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 1091 1091 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 1358 1358 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 1372 1372 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 1383 1383 N-linked (G1cNAc . . .) (Potential).
FT CARBOHYD 1768 1768 N-linked (G1cNAc . . .) (Potential).
FT VARSPLIC 207 207 I -> V (in isoform 2).
FT VARSPLIC 212 212 /FTId=VSP_050589.
FT VARSPLIC 212 212 N -> D (in isoform 2).
FT VARSPLIC 666 666 E -> EVKIDKAVRDS (in isoform 3).
FT VARSPLIC 666 666 /FTId=VSP_050591.
FT VARSPLIC 1275 1283 SLVSLIANA -> FLNLSGLI (in isoform 4).
FT VARSPLIC 1275 1283 Missing (in isoform 4).
FT VARSPLIC 1284 1980 /FTId=VSP_050592.
FT VARSPLIC 1284 1980 Missing (in isoform 4).
FT CONFLICT 5 5 L -> V (in Ref. 4).
FT CONFLICT 133 133 L -> M (in Ref. 1).
FT CONFLICT 257 257 L -> L (in Ref. 4).
FT CONFLICT 274 278 MGNLR -> HGEPS (in Ref. 4).
FT CONFLICT 453 453 T -> N (in Ref. 4).
FT CONFLICT 477 477 S -> F (in Ref. 4).
FT CONFLICT 483 483 L -> I (in Ref. 4).
FT CONFLICT 492 492 R -> S (in Ref. 4).
FT CONFLICT 504 504 S -> F (in Ref. 4).
FT CONFLICT 547 548 LL -> MF (in Ref. 4).

FT CONFLICT 1445 1445 V -> I (in Ref. 1).
 FT CONFLICT 1519 1519 V -> I (in Ref. 1).
 FT CONFLICT 1702 1702 T -> A (in Ref. 4).
 SQ SEQUENCE 1980 AA; 225279 MW; 0BFC7BF137FD4F0 CRC64;

Query Match 89.3%; Score 25; DB 1; Length 1980;
 Best Local Similarity 100.0%; Pred. No. 1.5e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFMWVIGNLVNLFLALLISF 28
 Db 956 VFMWVIGNLVNLFLALLISF 980

RESULT 19

088421 PRELIMINARY; PRT; 1988 AA.
 ID 088421
 AC 088421
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Voltage-gated sodium channel variant rRNA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=dorsal root ganglia;
 RX MEDLINE=98264329; PubMed=9603190;
 RA Dietrich P.S., McGilvern J.G., Delgado S.G., Koch B.D., Eglén R.M.,
 RA Hunter J.C., Sangameswaran L.;
 RT "Functional analysis of a voltage-gated sodium channel and its splice
 variant from rat dorsal root ganglia.";
 RL J. Neurochem. 70:2262-2272(1998).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; AF049240; AAC26015.1; -.
 DR HSRP; P04775; IBYV.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005248; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Decarboxylase2.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M_channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR008054; Na_channel18.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans; 4.
 DR Pfam; PF00612; IQ; 1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR PRINTS; PRO1667; NACHANNEL8.
 DR SMART; SM00015; IQ; 1.
 DR PROSITE; PS00878; ODR_DC_2_1; UNKNOWN 1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 1988 AA; 226186 MW; C1F7D87FDC366C9F CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1988;
 Best Local Similarity 100.0%; Pred. No. 1.6e-14;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFMWVIGNLVNLFLALLISF 28
 Db 964 VFMWVIGNLVNLFLALLISF 988

RESULT 20

015858 PRELIMINARY; PRT; 1977 AA.
 ID 015858
 AC 015858
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Sodium channel alpha subunit.
 GN Name=hNE-Na;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thyroid;
 RX MEDLINE=95237189; PubMed=7720699;
 RA Klugbauer N., Lacinova L., Flocke V., Hofmann F.;
 RT "Structure and functional expression of a new member of the
 RT tetrodotoxin-sensitive voltage-activated sodium channel family from
 RT human neuroendocrine cells.";
 RL EMBO J. 14:1084-1090(1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; X82835; CA58042.1; -.
 DR PIR; S54771; S54771.
 DR HSRP; P04775; IBYV.
 DR Genew; HGNC:10597; SCN9A.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
 DR GO; GO:0006814; P:sodium ion transport; TAS.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M_channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans; 4.
 DR Pfam; PF00612; IQ; 1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR SMART; SM00015; IQ; 1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 1977 AA; 225195 MW; 17D67C8C32BC15FB CRC64;

Query Match 82.1%; Score 23; DB 2; Length 1977;
 Best Local Similarity 100.0%; Pred. No. 1.1e-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 MWMVIGNLVNLFLALLISF 28
 Db 938 MWMVIGNLVNLFLALLISF 960

RESULT 21
 028644 PRELIMINARY; PRT; 1984 AA.
 ID 028644
 AC 028644
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Sodium channel alpha-subunit.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxId=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Sciatic nerve;
 RX MEDLINE=96074641; PubMed=7479931;

RA Belcher S.M., Zexillo C.A., Levenson R., Ritchie J.M., Howe J.R.;
 RT "Cloning of a sodium channel alpha subunit from rabbit Schwann
 cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL: U55238; AAA89159.1; -.
 DR HSSP: P04775; IBYI.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO: GO:0005261; F:cation channel activity; IEA.
 DR GO: GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO: GO:0006812; P:cation transport; IEA.
 DR GO: GO:0006814; P:sodium ion transport; IEA.
 DR InterPro: IPR001682; Ca/Na_pore.
 DR InterPro: IPR002111; Cat_channel_TrpL.
 DR InterPro: IPR000948; Ion_trans.
 DR InterPro: IPR005820; M_channel_nlg.
 DR InterPro: IPR001696; Na_channel.
 DR Pfam: PF00520; Ion_trans; 4.
 DR Pfam: PF06512; IQ; 1.
 DR Pfam: PF06512; Na_trans_assoc; 1.
 DR PRINTS: PR00170; NACHANNEL.
 DR SMART: SM00015; IQ; 1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 1984 AA; 225748 MW; 98F76860C9866AA0 CRC64;

Query Match 82.1%; Score 23; DB 2; Length 1984;
 Best Local Similarity 100.0%; Pred. No. 1.le-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 MMWVIGNLVYLNFLALILSSSF 28
 DB 946 MMWVIGNLVYLNFLALILSSSF 968

RESULT 22
 ID 008562; PRELIMINARY; PRT; 1984 AA.
 AC 008562;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE PNI (Voltage-gated sodium channel) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97188502; PubMed=9037087;
 RA Toledo-Arai J.J., Moss B.L., He Z.J., Kozowski A.G., Whisenand T.,
 Levenson S.R., Wolf J.J., Silos-Santiago I., Halegoua S., Mandel G.;
 RT "Identification of PNI, a predominant voltage-dependent sodium channel
 expressed principally in peripheral neurons.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:1527-1532(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97007982; PubMed=8854872;
 RA Kozak C.A., Sangameswaran L.;
 RT "Genetic mapping of the peripheral sodium channel genes, Scn9a and
 Scn10a, in the mouse.";
 RL Mamm. Genome 7:787-788(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Sangameswaran L., Fish L.M., Koch B.D., Rabert D.K., Delgado S.G.,
 RA Ilinskka M., Jakeman L.B., Novakovic S., Wong K., Sze P., Tzoumaka E.,
 RA Stewart G.R., Herman R.C., Chan H., Eglen R.M., Hunter J.C.;
 RT "A novel tetrodotoxin-sensitive, voltage-gated sodium channel
 expressed in rat and human dorsal root ganglia.";

RL J. Biol. Chem. 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL: U79568; AA850403.1; -.
 DR EMBL: AF000368; AA880701.1; -.
 DR HSSP: P04775; IBYI.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO: GO:0005261; F:cation channel activity; IEA.
 DR GO: GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO: GO:0006812; P:cation transport; IEA.
 DR GO: GO:0006814; P:sodium ion transport; IEA.
 DR InterPro: IPR001682; Ca/Na_pore.
 DR InterPro: IPR002111; Cat_channel_TrpL.
 DR InterPro: IPR000948; Ion_trans.
 DR InterPro: IPR005820; M_channel_nlg.
 DR InterPro: IPR001696; Na_channel.
 DR Pfam: PF00520; Ion_trans; 4.
 DR Pfam: PF06512; IQ; 1.
 DR Pfam: PF06512; Na_trans_assoc; 1.
 DR PRINTS: PR00170; NACHANNEL.
 DR SMART: SM00015; IQ; 1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 FT NON TER 1984 1984
 SQ SEQUENCE 1984 AA; 226037 MW; 386C38B9B5097091 CRC64;

Query Match 82.1%; Score 23; DB 2; Length 1984;
 Best Local Similarity 100.0%; Pred. No. 1.le-12;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 MMWVIGNLVYLNFLALILSSSF 28
 DB 948 MMWVIGNLVYLNFLALILSSSF 970

RESULT 23
 ID 080079; PRELIMINARY; PRT; 473 AA.
 AC 080079;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Sodium channel 6 (Fragment).
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OC NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lu Y., Lopezato G.F., Zakhon H.H.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY204537; AAC060425.1; -.
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0005261; F:cation channel activity; IEA.
 DR GO: GO:0006812; P:cation transport; IEA.
 DR InterPro: IPR001682; Ca/Na_pore.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR005820; M_channel_nlg.
 DR InterPro: IPR010526; Na_trans_assoc.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF06512; Na_trans_assoc; 1.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 FT NON TER 473 473
 FT NON TER 1
 SQ SEQUENCE 473 AA; 53617 MW; D922504FDCDF1B CRC64;
 Query Match 78.6%; Score 22; DB 2; Length 473;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MWMVIGNLVVNLFLALLSSP 28
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 DB 12 MWMVIGNLVVNLFLALLSSP 33

RESULT 24

Q800U1 PRELIMINARY; PRT; 488 AA.

ID 0800U1
 AC 0800U1;
 DT 01-JUN-2003 (TEMBLrel. 24, Created)
 DT 01-JUN-2003 (TEMBLrel. 24, last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, last annotation update)
 DE Sodium channel 4 (Fragment).
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OC NCB1_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lu Y., Lopreato G.F., Zakon H.H.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY204535; AA060423.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans.1.
 DR Pfam; PF06512; Na_trans_assoc.1.
 DR Ion transport; Ionic channel; Transmembrane; Transport.
 KM NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 488 AA; 55100 MW; 379A1BAA105F3A8F CRC64;

Query Match 78.6%; Score 22; DB 2; Length 488;
 Best Local Similarity 100.0%; Pred.No. 3.1e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MWMVIGNLVVNLFLALLSSP 28
 |||||
 DB 12 MWMVIGNLVVNLFLALLSSP 33

RESULT 25

Q90227 PRELIMINARY; PRT; 744 AA.

ID 090227
 AC 090227;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, last annotation update)
 DE Sodium channel 4 (Fragment).
 OS Sternopygus macrurus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
 OC Sternopygidae; Sternopygus.
 OC NCB1_TaxID=77841;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21310016; PubMed=11416226;
 RA Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
 RA Wilcox T.P., Zakon H.H.;
 RT "Evolution and divergence of sodium channel genes in vertebrates";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
 DR EMBL; AF378142; AA05440.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.

DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans.2.
 DR Pfam; PF06512; Na_trans_assoc.1.
 DR Ion transport; Ionic channel; Transmembrane; Transport.
 KM NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 744 AA; 84557 MW; B0D6E7B203893C28 CRC64;

Query Match 78.6%; Score 22; DB 2; Length 744;
 Best Local Similarity 100.0%; Pred.No. 4.4e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 MWMVIGNLVVNLFLALLSSP 28
 |||||
 DB 184 MWMVIGNLVVNLFLALLSSP 205

Search completed: January 27, 2005, 17:51:32
 Job time : 94.5 secs

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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:50 ; Search time 22.5 Seconds
(without alignments)
82.529 Million cell updates/sec

Title: US-10-608-584-13

Perfect score: 28

Sequence: 1 CLTVFMVWVIGNLVNLFLALLSSP 28

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

1: Issued Patents AA: *
2: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/6C_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	2005	3	US-08-836-325-7
2	28	100.0	2005	4	US-09-457-571-7
3	25	89.3	1976	3	US-09-024-020B-9
4	25	89.3	1976	3	US-09-425-043-9
5	25	89.3	1978	3	US-09-024-020B-3
6	25	89.3	1978	3	US-09-425-043-3
7	25	89.3	1988	3	US-09-024-020B-4
8	25	89.3	1988	3	US-09-425-043-4
9	23	82.1	1835	3	US-08-836-325-15
10	23	82.1	1835	3	US-09-457-571-15
11	23	82.1	1969	4	US-08-836-325-16
12	23	82.1	1969	4	US-09-457-571-16
13	23	82.1	1977	4	US-09-976-594-757
14	23	82.1	1977	4	US-09-919-039-167
15	23	82.1	1984	4	US-08-836-325-10
16	23	82.1	1984	4	US-09-457-571-10
17	23	82.1	1989	3	US-08-836-325-11
18	23	82.1	1989	3	US-08-836-325-12
19	23	82.1	1989	4	US-09-457-571-11
20	23	82.1	1989	4	US-09-457-571-12
21	22	78.6	1836	4	US-10-162-012-24
22	22	78.6	1836	4	US-09-562-737-81
23	21	75.0	2016	4	US-09-634-920-4
24	21	75.0	2016	4	US-09-514-907A-2
25	21	75.0	2016	4	US-09-896-994-2
26	21	75.0	2016	4	US-09-840-125-4
27	17	60.7	1820	3	US-07-998-289B-8

28	17	60.7	2100	2	US-08-808-793-23	Sequence 23, Appl
29	17	60.7	2100	3	US-08-772-512A-19	Sequence 19, Appl
30	17	60.7	2105	3	US-08-808-793-3	Sequence 3, Appl
31	17	60.7	2105	3	US-08-772-512A-3	Sequence 3, Appl
32	16	57.1	813	4	US-08-836-325-8	Sequence 8, Appl
33	16	57.1	813	4	US-09-457-571-8	Sequence 8, Appl
34	16	57.1	1011	3	US-08-836-325-2	Sequence 2, Appl
35	16	57.1	1011	3	US-09-457-571-2	Sequence 2, Appl
36	12	42.9	2104	2	US-08-808-793-4	Sequence 4, Appl
37	12	42.9	2104	3	US-08-772-512A-4	Sequence 4, Appl
38	9	32.1	1024	4	US-09-562-737-82	Sequence 82, Appl
39	9	32.1	1024	4	US-09-562-737-83	Sequence 83, Appl
40	9	32.1	1024	4	US-09-562-737-84	Sequence 84, Appl
41	9	32.1	1024	4	US-09-562-737-85	Sequence 85, Appl
42	9	32.1	1024	4	US-09-562-737-86	Sequence 86, Appl
43	9	32.1	1024	4	US-09-562-737-87	Sequence 87, Appl
44	9	32.1	1024	4	US-09-562-737-88	Sequence 88, Appl
45	9	32.1	1024	4	US-09-562-737-89	Sequence 89, Appl
46	9	32.1	1024	4	US-09-562-737-90	Sequence 90, Appl
47	9	32.1	1956	3	US-08-843-417-2	Sequence 2, Appl
48	9	32.1	1956	3	US-08-843-417-10	Sequence 10, Appl
49	9	32.1	1956	4	US-09-527-013-2	Sequence 2, Appl
50	9	32.1	1956	4	US-09-527-013-10	Sequence 10, Appl
51	9	32.1	1957	4	US-08-669-656A-2	Sequence 2, Appl
52	9	32.1	1957	4	US-08-669-656A-8	Sequence 8, Appl
53	9	32.1	2132	4	US-08-669-656A-6	Sequence 6, Appl
54	8	28.6	501	1	US-08-331-394-4	Sequence 4, Appl
55	8	28.6	501	1	US-08-250-858-4	Sequence 4, Appl
56	8	28.6	501	1	US-08-446-915-4	Sequence 4, Appl
57	8	28.6	501	2	US-08-744-119-4	Sequence 4, Appl
58	8	28.6	501	4	US-08-779-599-4	Sequence 4, Appl
59	8	28.6	501	5	PCT-US95-06639-4	Sequence 4, Appl
60	6	25.0	104	6	US-08-833-488B-4	Sequence 4, Appl
61	7	25.0	197	3	US-08-833-488B-9	Sequence 9, Appl
62	7	25.0	197	3	US-08-833-488B-28	Sequence 28, Appl
63	7	25.0	197	3	US-08-833-488B-14	Sequence 14, Appl
64	7	25.0	199	3	US-08-833-488B-14	Sequence 14, Appl
65	7	25.0	204	6	US-08-833-488B-14	Sequence 14, Appl
66	7	25.0	253	3	US-08-833-488B-20	Sequence 20, Appl
67	7	25.0	431	4	US-09-592-998C-9	Sequence 9, Appl
68	7	25.0	431	4	US-09-592-998C-10	Sequence 10, Appl
69	7	25.0	435	4	US-09-446-861-127	Sequence 127, Appl
70	7	25.0	461	3	US-09-122-210-2	Sequence 2, Appl
71	7	25.0	461	3	US-09-443-681-2	Sequence 2, Appl
72	7	25.0	573	4	US-09-643-657-18	Sequence 18, Appl
73	7	25.0	586	4	US-10-140-002-46	Sequence 46, Appl
74	7	25.0	591	4	US-09-643-657-3	Sequence 3, Appl
75	7	25.0	633	2	US-08-726-770-3	Sequence 3, Appl
76	7	25.0	728	4	US-09-252-991A-23738	Sequence 23738, A
77	7	25.0	1023	4	US-10-140-002-200	Sequence 200, Appl
78	7	25.0	1233	4	US-09-354-147C-7	Sequence 7, Appl
79	7	25.0	1233	4	US-09-354-147C-8	Sequence 8, Appl
80	7	25.0	1498	2	US-08-404-531B-28	Sequence 28, Appl
81	7	25.0	1498	2	US-08-404-531B-29	Sequence 29, Appl
82	7	25.0	1498	3	US-08-476-900A-28	Sequence 28, Appl
83	7	25.0	1498	3	US-08-476-900A-29	Sequence 29, Appl
84	7	25.0	1498	3	US-08-488-566A-28	Sequence 28, Appl
85	7	25.0	1498	3	US-08-488-566A-29	Sequence 29, Appl
86	7	25.0	1580	3	US-08-726-320-1	Sequence 1, Appl
87	7	25.0	1580	3	US-09-208-716-1	Sequence 1, Appl
88	7	25.0	1581	2	US-08-404-531B-6	Sequence 6, Appl
89	7	25.0	1581	3	US-08-476-900A-6	Sequence 6, Appl
90	7	25.0	1581	3	US-08-488-566A-6	Sequence 6, Appl
91	7	25.0	1581	3	US-08-726-320-3	Sequence 3, Appl
92	7	25.0	1581	3	US-08-726-320-4	Sequence 4, Appl
93	7	25.0	1581	3	US-09-208-716-3	Sequence 3, Appl
94	7	25.0	1581	3	US-09-208-716-4	Sequence 4, Appl
95	7	25.0	1582	2	US-08-404-531B-9	Sequence 9, Appl
96	7	25.0	1582	3	US-08-476-900A-9	Sequence 9, Appl
97	7	25.0	1582	3	US-08-488-566A-9	Sequence 9, Appl
98	7	25.0	1582	3	US-08-726-320-5	Sequence 5, Appl
99	7	25.0	1582	3	US-09-208-716-5	Sequence 5, Appl
100	7	25.0	1765	4	US-09-354-147C-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-08-836-325-7
Sequence 7, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Haleboua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-325-7

Query Match 100.0%; Score 28; DB 3; Length 2005;

Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTVFMWVWVIGNLVYVNLFLALLSSSF 28

Db 959 CLTVFMWVWVIGNLVYVNLFLALLSSSF 986

RESULT 2

US-09-457-571-7
Sequence 7, Application US/09457571
Patent No. 6703486

GENERAL INFORMATION:

APPLICANT: Mandel, Gail
APPLICANT: Haleboua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-457-571-7

Query Match 100.0%; Score 28; DB 4; Length 2005;

Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLTVFMWVWVIGNLVYVNLFLALLSSSF 28

Db 959 CLTVFMWVWVIGNLVYVNLFLALLSSSF 986

RESULT 3

US-09-024-020B-9
Sequence 9, Application US/09024020B
Patent No. 6030810
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE

TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1976 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-020B-9

Query Match 89.3%; Score 25; DB 3; Length 1976;
Best Local Similarity 100.0%; Pred. No. 8.6e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFMWVYIGNLVNLFALILSSP 28
Db 952 VFMWVYIGNLVNLFALILSSP 976

RESULT 4
US-09-425-043-9
Sequence 9, Application US/09425043
Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1976 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-425-043-9

Query Match 89.3%; Score 25; DB 3; Length 1976;
Best Local Similarity 100.0%; Pred. No. 8.6e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFMWVYIGNLVNLFALILSSP 28
Db 952 VFMWVYIGNLVNLFALILSSP 976

RESULT 5
US-09-024-020B-3
Sequence 3, Application US/09024020B
Patent No. 6030810
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 1978 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-020B-3

Query Match 89.3%; Score 25; DB 3; Length 1978;
Best Local Similarity 100.0%; Pred. No. 8.6e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VFMMVWVIGNLVYINLFLALLISSF 28
DB 954 VFMMVWVIGNLVYINLFLALLISSF 978

RESULT 6
US-09-425-043-3
Sequence 3, Application US/09425043
Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1978 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-425-043-3

Query Match 89.3%; Score 25; DB 3; Length 1978;
Best Local Similarity 100.0%; Pred. No. 8.6e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VFMMVWVIGNLVYINLFLALLISSF 28
DB 954 VFMMVWVIGNLVYINLFLALLISSF 978

RESULT 7
US-09-024-020B-4
Sequence 4, Application US/09024020B
Patent No. 6030810
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-020B-4

Query Match 89.3%; Score 25; DB 3; Length 1988;
Best Local Similarity 100.0%; Pred. No. 8.6e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 VFMMVWVIGNLVYINLFLALLISSF 28
DB 964 VFMMVWVIGNLVYINLFLALLISSF 988

RESULT 8
US-09-425-043-4
Sequence 4, Application US/09425043
Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:


```

ADDRESS: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 852-5322
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-425-043-4

Query Match      89.3%; Score 25; DB 3; Length 1988;
Best Local Similarity 100.0%; Pred. No. 8,66-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VPMVMVIGNLVNLFALLISSF 28
DB 964 VPMVMVIGNLVNLFALLISSF 988

RESULT 9
US-08-836-325-15
Sequence 15, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational,
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325

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FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-836-325-15

Query Match      82.1%; Score 23; DB 3; Length 1835;
Best Local Similarity 100.0%; Pred. No. 6,7e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MMVMVIGNLVNLFALLISSF 28
DB 882 MMVMVIGNLVNLFALLISSF 904

RESULT 10
US-09-457-571-15
Sequence 15, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational,
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401

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FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1835 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-457-571-15

Query Match 82.1%; Score 23; DB 4; Length 1835;
Best Local Similarity 100.0%; Pred. No. 6,7e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 MMVVVIGNLVVNLFLALLSSF 28
Db 882 MMVVVIGNLVVNLFLALLSSF 904

RESULT 11
US-08-836-325-16
Sequence 16, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-16

Query Match 82.1%; Score 23; DB 3; Length 1969;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 MMVVVIGNLVVNLFLALLSSF 28
Db 938 MMVVVIGNLVVNLFLALLSSF 960

RESULT 12
US-09-457-571-16
Sequence 16, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-457-571-16

Query Match 82.1%; Score 23; DB 4; Length 1969;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 MMWVIGNLVYVNLFLALLSSSF 28
Db 938 MMWVIGNLVYVNLFLALLSSSF 960

RESULT 13
US-09-976-594-757
Sequence 757, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LAYER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
NUMBER OF SEQ ID NOS: 2000-10-12
SOFTWARE: PERL Program
SEQ ID NO 757
LENGTH: 1977
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 1719478CD1
US-09-976-594-757

Query Match 82.1%; Score 23; DB 4; Length 1977;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 MMWVIGNLVYVNLFLALLSSSF 28
Db 938 MMWVIGNLVYVNLFLALLSSSF 960

RESULT 14
US-09-919-039-367
Sequence 367, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaeber, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
PRIOR FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
NUMBER OF SEQ ID NOS: 2000-07-28
SOFTWARE: PERL Program
SEQ ID NO 367
LENGTH: 1977
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6727066 1719478CD1
US-09-919-039-367

Query Match 82.1%; Score 23; DB 4; Length 1977;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 MMWVIGNLVYVNLFLALLSSSF 28
Db 938 MMWVIGNLVYVNLFLALLSSSF 960

RESULT 15
US-08-836-325-10
Sequence 10, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-10

Query Match 82.1%; Score 23; DB 3; Length 1984;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 MMWVIGNLVYVNLFLALLSSSF 28
Db 948 MMWVIGNLVYVNLFLALLSSSF 970

RESULT 16
US-09-457-571-10
Sequence 10, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:

APPLICANT: Mandel, Gail
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-457-571-10

Query Match 82.1%; Score 23; DB 4; Length 1984;
Best Local Similarity 100.0%; Pred.No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MMWVIGNLVVNLFLALLISF 28
DB 948 MMWVIGNLVVNLFLALLISF 970

RESULT 17
US-08-836-325-11
Sequence 11, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halsegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-836-325-11

Query Match 82.1%; Score 23; DB 3; Length 1989;
Best Local Similarity 100.0%; Pred.No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MMWVIGNLVVNLFLALLISF 28
DB 949 MMWVIGNLVVNLFLALLISF 971

RESULT 18
US-08-836-325-12
Sequence 12, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halsegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-836-325-12

Query March 82.1%; Score 23; DB 3; Length 1989;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MMWVIGNLVVNLFLALLSSP 28
DB 949 MMWVIGNLVVNLFLALLSSP 971

RESULT 19
US-09-457-571-11
Sequence 11, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325

FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-457-571-11

Query March 82.1%; Score 23; DB 4; Length 1989;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MMWVIGNLVVNLFLALLSSP 28
DB 949 MMWVIGNLVVNLFLALLSSP 971

RESULT 20
US-09-457-571-12
Sequence 12, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA: 08/34,029
APPLICATION NUMBER: 02-NOV-1994
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein

Query Match	82.1%	Coverage	82.1%	Indels	0	Gaps	0
Best Local Similarity	100.0%	Pred. No.	7.2e-14	Indels	0	Gaps	0
Matches	23	Mismatches	0	Indels	0	Gaps	0
	Conservative						

QY 9 971
949 MVMVIGNLVTLNLFALLSSF 971

RESULT 21
US-10-162-012-24
Application US/10162012

APPLICANT: CUTTIS, ROYAL
APPLICANT: SLOS-SANTAGLO, IMMACULADA
APPLICANT: GU, WEI
TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
FILE REFERENCE: 10448-19001
CURRENT APPLICATION NUMBER: US/10/162,012
CURRENT FILING DATE: 2002-06-04
CURRENT FILING DATE: US 60/209,845
PRIOR APPLICATION NUMBER: 2000-06-06
PRIOR FILING DATE: US 09/875,321
PRIOR APPLICATION NUMBER: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: PCT/US01/18340
PRIOR FILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/209,257
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875,423
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18398
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,238
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: US 09/875,363
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: PCT/US01/18247
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/227,068
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: US 09/928,530
PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: PCT/US01/25475
PRIOR FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: US 60/226,770
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: US 09/934,421
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: PCT/US01/26096
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/279,281
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 10/109,029

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PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: PCT/US02/09728
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/290,288
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US (not assigned)
PRIOR FILING DATE: 2002-05-13
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 1836
TYPE: PRT
ORGANISM: Homo sapiens
US-10-162-012-24

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[illegible]

QY ||||| 784 MWMVIGNLVNLFTALLSSP 805

RESULT 22
US-09-562-737-81
Sequence 81, Application US/09562737

GENERAL INFORMATION:
; Herz, Joachim
; APPLICANT: Michael
; Gotthardt, Michael
; APPLICANT: Professor Signaling Pathways

FILE REFERENCE: US/09/562, 751
CURRENT APPLICATION NUMBER: 2000-05-01
FILING DATE: 2000-05-01

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;
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
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; Artificial Sequence: Synthetic
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; ORGANISM: Artificial Sequence: Synthetic
FEATURES:
            Description of Artificial Sequence: Synthetic

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OTHER INFO.....	
US-09-562-737-81	
75 0%:	Score 21; DB 4; Length 1024;
	0 30-12.

Best Local Simulation	0;	MisMatch
Matches	21;	Conservative
		28

918 VMVIGNLVNLFLALLSSF 938

RESULT 23
US-09-634-920-4
US/09634920

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1 Patent no.:
2 GENERAL INFORMATION:
3 APPLICANT: Solawski, Igor
4 APPLICANT: Keating, Mark T.
5 TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME
6 TITLE OF INVENTION: SCN5A AND METHODS FOR DETECTING
7 TITLE OF INVENTION: 2323-155
8 FILE REFERENCE: US/09/634,920
9 CURRENT APPLICATION NUMBER: 2000-08-09
10 CURRENT FILING DATE: 2000-08-09
11 PRIOR APPLICATION NUMBER: 60/199,057
12 PRIOR FILING DATE: 2000-03-17
13 PRIOR APPLICATION NUMBER: 60/147,400
14 PRIOR FILING DATE: 1999-08-09
15 NUMBER OF SEQ ID NOS: 4
16 SOFTWARE: PatentIn Ver. 2

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SEQ ID NO 4
LENGTH: 2016
TYPE: PRT
ORGANISM: Homo sapiens
US-09-634-920-4

Query Match 75.0%; Score 21; DB 3; Length 2016;
Best Local Similarity 100.0%; Pred. No. 6,1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VMVIGNLVNLFLLALLSSF 28
Db 922 VMVIGNLVNLFLLALLSSF 942

RESULT 24
US-09-514-907A-2
Sequence 2, Application US/09514907A
Patent No. 6567705
GENERAL INFORMATION:

APPLICANT: Kenneth B. Stokes
TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL
SENSING BY CARDIAC PACEMAKERS THROUGH
GENETIC TREATMENT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705stris LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,907A
FILING DATE: 08-Feb-2000
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown

US-09-514-907A-2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 75.0%; Score 21; DB 4; Length 2016;
Best Local Similarity 100.0%; Pred. No. 6,1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VMVIGNLVNLFLLALLSSF 28
Db 922 VMVIGNLVNLFLLALLSSF 942

RESULT 25
US-09-896-994-2
Sequence 2, Application US/09896994
Patent No. 6665563
GENERAL INFORMATION:
APPLICANT: Ken Stokes

Joe e Morissette
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/896,994
FILING DATE: 02-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/514,907
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown

US-09-896-994-2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 75.0%; Score 21; DB 4; Length 2016;
Best Local Similarity 100.0%; Pred. No. 6,1e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VMVIGNLVNLFLLALLSSF 28
Db 922 VMVIGNLVNLFLLALLSSF 942

Search completed: January 27, 2005, 17:54:18
Job time : 23.5 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 27, 2005, 17:33:04 ; Search time 86.5 Seconds

(without alignments)
116.120 Million cell updates/sec

Title: US-10-608-584-19

Perfect score: 28
Sequence: 1 MYLFFVIFIFIGSFITLNLFIGIILDNF 28Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : A Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	28	100.0	1836	7	ADP59630 Human Pro
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6	28	100.0	1836	8	ADP17412 Human scd
7	28	100.0	1855	7	ADB78597 Human scd
8	28	100.0	1950	7	ADB78607 Human scd
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12	28	100.0	1951	8	ADP59628 Rat Prote
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26	28	100.0	2005	7	ADB78605 Human scd
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98	28	100.0	2005	7	AA899636 Human scd

99 21 75.0 1978 7 ADE54549
100 21 75.0 1989 2 AAR9640

AD65459 Human Pro
Aar9640 Periphra

ALIGNMENTS

RESULT 1
ADFA5244
ID ADF45244 standard; protein; 280 AA.

XX ADF45244;

XX 26-FEB-2004 (first entry)

DE Human sodium channel alpha subunit amino acid sequence.

XX human; cation channel; INPIONCH05; INPIONCH06; tetrameric cation channel;
XX antifertility; neuroprotective; cardiovascular; immunosuppressive;
XX cerebroprotective; vasotropic; contraceptive; vaccine; infertility;
XX neurological disorder; cardiovascular disorder; autoimmune disease;
XX stroke; stroke-related disorder; pathological condition; calcium channel.

XX Homo sapiens.

XX WO200309865-A1.

XX 04-DEC-2003.

XX 23-MAY-2003; 2003WO-GB002270.

XX 24-MAY-2002; 2002GB-00012067.

XX (INPH-) INPHARMATICA LTD.

XX Lobley AE, Michalovich D, Allen KE, Reynolds L, Pierron VN;

XX WPI; 2004-053233/05.

XX New INPIONCH05 and INPIONCH06 polypeptides, useful as a contraceptive
XX agent, or for diagnosing and treating a disease or disorder, e.g.
XX infertility, neurological disorder, cardiovascular disorder, autoimmune
XX disease or stroke.

XX Example 1; Fig 2; 96pp; English.

XX The present invention describes cation channel polypeptides (I), termed
XX INPIONCH05 and INPIONCH06. Also described: (1) a purified nucleic acid
XX molecule (II), which: (a) encodes (I); or (b) hybridizes under high
XX stringency conditions with the nucleic acid molecule of (a); (2) a vector
XX comprising (I); (3) a host cell transformed with the vector; (4) a
XX tetrameric cation channel comprising (I); (5) a ligand which binds
XX specifically to, and which preferably inhibits the activity of (I) or the
XX tetrameric cation channel; (6) a compound that either increases or
XX decreases the level of expression or activity of (I) or the tetrameric
XX cation channel; (7) a method of diagnosing a disease in a patient; (8) a
XX pharmaceutical composition comprising (I), (II), vector, host cell,
XX comprising (I) or (II); (10) a method of treating a disease in a patient;
XX (11) a method of monitoring the therapeutic treatment of disease in a
XX patient; (12) a method for the identification of a compound that is
XX effective in the treatment and/or diagnosis of a disease/disorder; (13)
XX an array of nucleic acid molecules, at least one of which is (II), or one
XX or more antibodies that bind to (I) or to the tetrameric cation channel,
XX antibody and (I) or tetrameric cation channel; (14) a transgenic or
XX knock-out non-human animal that has been transformed to express higher,
XX lower or absent levels of (I); and (15) a method for screening for a
XX compound effective to treat a disease or disorder. (I) has
XX antifertility, neuroprotective, cardiovascular, immunosuppressive,
XX cerebroprotective, vasotropic and contraceptive activities, and can be
XX used in vaccines. (I), (II), vectors, tetrameric cation channels,
XX ligands, compounds, or compositions of the present invention may be used

CC as contraceptive agents, preferably a non-hormonal contraceptive agent,
CC in therapy or diagnosis of a disease or disorder, or in manufacturing a
CC medicament for the treatment of a disease or disorder, e.g. infertility,
CC neurological disorder, cardiovascular disorder, autoimmune disease,
CC stroke, stroke-related disorders or other pathological condition. (I) is
CC useful as a cation channel or a calcium channel. (I) or the tetrameric
CC cation channel is useful as a sperm-specific CatSper channel. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 280 AA;

Query Match 100.0%; Score 28; DB 8; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.4e-21;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLYFVIRLPGSPFTNLFGVITIDNF 28
DB 246 MLYFVIRLPGSPFTNLFGVITIDNF 273

RESULT 2
ADB78596

XX ADB78596 standard; protein; 1795 AA.

XX ADB78596;

XX 04-DEC-2003 (first entry)

XX Human sodium channel subunit mutant SEQ ID NO:140.

XX mutein; mutant; ion channel; ion channel subunit; ICS; nootropic;
XX neuroprotective; inotropic; antipyretic; antihypertensive; antimigraine;
XX antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;
XX nephrotoxic; antidiabetic; ophthalmological; epilepsy;
XX ion channel dysfunction; human.

XX Synthetic.

XX Homo sapiens.

XX WO2003008574-A1.

XX 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.

XX 18-JUL-2001; 2001AU-00006452.

XX 05-MAR-2002; 2002AU-0000910.

XX 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

XX (WALL-) WALLACE R W.

XX Muller JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE,

XX Berkovic SF, Scheffer IE;

XX WPI; 2003-239332/23.

XX N-PSDB; ADB78635.

XX Claim 13; SEQ ID NO 140; 106pp; English.

XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has nootropic, neuroprotective, inotropic, antipyretic,
XX antihypertensive, antiparkinsonian, analgesic, nephrotoxic, antidiabetic, and

ophthalmological activity. A polynucleotide of the invention acts as an ion channel agonist, or ion channel antagonist. The methods, isolated nucleic acids, polypeptides, antibody, selective agonist, antagonist or modulator of an ion channel, cells and genetically modified non-human animal, are useful for the diagnosis and treatment of epilepsy and/or a disorder associated with ion channel dysfunction, such as hyper- or hypokalemia, periodic paralysis, myotonia, malignant hyperthermia, myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety, depression, phobic obsessive syndrome, neuropathic pain, inflammatory pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease, Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic fibrosis, congenital stationary night blindness and total colour blindness. The present sequence represents a mutant protein of the invention. The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 1795 AA;

Query Match 100.0%; Score 28; DB 7; Length 1795;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MYLVFVIFIFGSPFTLNLFICVIIDNF 28
1459 MYLVFVIFIFGSPFTLNLFICVIIDNF 1486

RESULT 3
ADE57388 ID ADE57388 standard; protein; 1836 AA.

AC ADE57388;

DT 29-JAN-2004 (first entry)

DE Human Protein XP_008249, SEQ ID NO 3249.

Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNL; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002MO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; XP_008249.

PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence

which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNL)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

Sequence 1836 AA;

Query Match 100.0%; Score 28; DB 7; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MYLVFVIFIFGSPFTLNLFICVIIDNF 28
1271 MYLVFVIFIFGSPFTLNLFICVIIDNF 1298

RESULT 4
ADE59630 ID ADE59630 standard; protein; 1836 AA.

AC ADE59630;

DT 29-JAN-2004 (first entry)

DE Human Protein XP_008249, SEQ ID NO 5526.

Human; pain; neuronal tissue; gene therapy;
spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNL; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002MO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; XP_008249.

PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 1836 AA;

Query Match 100.0%; Score 28; DB 7; Length 1836;
 Best Local Similarity 100.0%; Pred. No. 1.3e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MYLFFVFIIFGSPFTNLFIQVITIDNF 28
 Db 1271 MYLFFVFIIFGSPFTNLFIQVITIDNF 1298

RESULT 5
 ADE63029
 ID ADE63029 standard; protein; 1836 AA.
 XX
 AC ADE63029;

DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein XP_008249, SEQ ID NO 8963.
 XX

KM Human; pain; neuronal tissue; gene therapy;
 KM spinal segmental nerve injury; chronic constriction injury; CCI;
 KM spared nerve injury; SNI; Chung.
 XX

OS Homo sapiens.
 XX

PN WO2003016475-A2.
 XX

PD 27-FEB-2003.
 XX

PF 14-AUG-2002; 2002WO-US025765.
 XX

PR 14-AUG-2001; 2001US-0312147P.
 XX

PR 01-NOV-2001; 2001US-0346382P.
 XX

PR 26-NOV-2001; 2001US-0333347P.
 XX

PA (GENO) GEN HOSPITAL CORP.
 XX

PA (FARB) BAYER AG.
 XX

PI Woolf C, D'urso D, Befort K, Costigan M,
 XX WPI; 2003-268312/26.
 DR GENBANK; XP_008249.
 XX

PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX

PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 1836 AA;

Query Match 100.0%; Score 28; DB 7; Length 1836;
 Best Local Similarity 100.0%; Pred. No. 1.3e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MYLFFVFIIFGSPFTNLFIQVITIDNF 28
 Db 1271 MYLFFVFIIFGSPFTNLFIQVITIDNF 1298

RESULT 6
 ADQ17412
 ID ADQ17412 standard; protein; 1836 AA.
 XX
 AC ADQ17412;

DT 26-AUG-2004 (first entry)
 XX

DE Human soft tissue sarcoma-upregulated protein - SEQ ID 229.
 XX

KM soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 KM

OS Homo sapiens.
 XX

PN WO2004048938-A2.
 XX

PD 10-JUN-2004.
 XX

PF 26-NOV-2003; 2003WO-US038193.
 XX

PR 26-NOV-2002; 2002US-0429739P.
 XX

PA (PROT-) PROTEIN DESIGN LABS INC.
 XX

PA Aziz N, Ginsburg WM, Zlotnick A;
 XX WPI; 2004-441208/41.
 DR
 XX

PT Early detection of soft tissue sarcoma comprises determining expression

PT of a gene in a first soft tissue sample and a normal soft tissue sample
PT and comparing the gene expression, also useful in treating soft tissue
PT sarcoma.
XX
PS Example 2; SEQ ID NO 229; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in both soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 1836 AA;
XX
Query Match 100.0%; Score 28; DB 8; Length 1836;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MYLVFVFIIFGSPFTLNLFIGVITDNF 28
DB 1271 MYLVFVFIIFGSPFTLNLFIGVITDNF 1298
XX
RESULT 7
ADB78597
ID ADB78597 standard; protein; 1855 AA.
XX
AC ADB78597;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:141.
XX
KM mutein; mutant; ion channel; ion channel subunit; ICS; neurotropic;
KM neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KM antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KM nephrotoxic; antidiabetic; ophthalmological; epilepsy;
KM ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-0000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
XX
XX WPI; 2003-23932/23.
XX
XX N-PSDB; ADB78636.
XX
PT Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.

XX
PS Claim 13; SEQ ID NO 141; 106pp; English.
XX
CC The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has neurotropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotoxic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonia, malignant hyperthermia,
CC myaesthesia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 1855 AA;
XX
Query Match 100.0%; Score 28; DB 7; Length 1855;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MYLVFVFIIFGSPFTLNLFIGVITDNF 28
DB 1459 MYLVFVFIIFGSPFTLNLFIGVITDNF 1486
XX
RESULT 8
ADB78607
ID ADB78607 standard; protein; 1950 AA.
XX
AC ADB78607;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human sodium channel subunit mutant SEQ ID NO:151.
XX
KM mutein; mutant; ion channel; ion channel subunit; ICS; neurotropic;
KM neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
KM antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KM nephrotoxic; antidiabetic; ophthalmological; epilepsy;
KM ion channel dysfunction; human.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO2003008574-A1.
XX
PD 30-JAN-2003.
XX
PF 08-JUL-2002; 2002WO-AU000910.
XX
PR 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-0000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
PA (BION-) BIONOMICS LTD.
PA (WALL/) WALLACE R W.
XX
PI Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

PI Berkovic SF, Scheffer IE;
 CC WPI; 2003-239332/23.
 DR N-PSDB; ADB78646.
 XX
 PT Identifying predisposition to an ion channel dysfunction, such as
 CC periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
 PT schizophrenia, anxiety and depression, by detecting encoding-gene
 PT mutation events.
 XX
 PS Claim 13; SEQ ID NO 151; 106pp; English.

CC The invention relates to a novel method for identifying a subject
 CC predisposed to a disorder associated with ion channel dysfunction. The
 CC method comprises ascertaining if at least one of the genes encoding ion
 CC channel subunits (ICS) has undergone a mutation event so that a cDNA
 CC derived from the subject has any of 134 nucleotide sequences. The method
 CC of the invention has nootropic, neuroprotective, inotropic, antihypertic,
 CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
 CC neuroleptic, tranquiliser, analgesic, nephrotoxic, antidiabetic, and
 CC ophthalmological activity. A polynucleotide of the invention acts as an
 CC ion channel agonist, or ion channel antagonist. The methods, isolated
 CC modulator of an ion channel, antibody, selective agonist, antagonist or
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemia, cardiac arrhythmias, myotonias, malignant hyperthermia,
 CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
 CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
 XX
 SQ Sequence 1950 AA;

Query Match 100.0%; Score 28; DB 7; Length 1950;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLFFVFIIFGSPFTLNLFIVITDNF 28
 DB 1394 MYLFFVFIIFGSPFTLNLFIVITDNF 1421

RESULT 9
 AAB99678
 ID AAB99678 standard; protein; 1951 AA.
 AC AAB99678;
 XX
 DT 04-SEP-2001 (first entry)

XX Human adult form of SCN3A protein sequence SEQ ID NO:67.
 XX
 DE Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
 KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
 KM anticonvulsant; neuroprotective.
 XX
 OS Homo sapiens.

XX WO200138564-A2.
 XX
 XX 31-MAY-2001.
 PD
 XX 24-NOV-2000; 2000WO-CA001404.
 PF
 XX 26-NOV-1999; 99US-0167623P.
 PR
 XX

PA (UTMC-) UNIV MCGILL.
 XX
 XX Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
 DR WPI; 2001-355945/37.
 DR N-PSDB; AAH55823.
 XX
 PT Determining a predisposition to epilepsy and/or development of epilepsy
 CC comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
 PT variant, equivalent, or mutation which shows a linkage disequilibrium.
 XX
 PS Disclosure; Page 157-165; 268pp; English.

CC The present invention describes a method (M1) of determining an
 CC individual's predisposition to epilepsy and/or development of epilepsy,
 CC as well as predicting the individual's response to medication. The method
 CC comprises determining the genotype of at least one gene selected from
 CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent or mutation which
 CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
 CC channel genes located on chromosome 2. The idiopathic generalised
 CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
 CC q31. Compounds identified as modulators of the biological activity of
 CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
 CC or other neurological disorders. They have anticonvulsant and
 CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
 CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
 CC oligonucleotides and proteins given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 1951 AA;

Query Match 100.0%; Score 28; DB 4; Length 1951;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLFFVFIIFGSPFTLNLFIVITDNF 28
 DB 1395 MYLFFVFIIFGSPFTLNLFIVITDNF 1422

RESULT 10
 AAB99679
 ID AAB99679 standard; protein; 1951 AA.
 AC AAB99679;
 XX
 DT 04-SEP-2001 (first entry)

XX Human neonatal form of SCN3A protein sequence SEQ ID NO:68.
 XX
 DE Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
 KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
 KM anticonvulsant; neuroprotective.
 XX
 OS Homo sapiens.

XX WO200138564-A2.
 XX
 XX 31-MAY-2001.
 PD
 XX 24-NOV-2000; 2000WO-CA001404.
 PF
 XX 26-NOV-1999; 99US-0167623P.
 PR
 XX (UTMC-) UNIV MCGILL.
 PA

XX Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
 DR WPI; 2001-355945/37.
 DR N-PSDB; AAH55824.
 XX
 PT

Determining a predisposition to epilepsy and/or development of epilepsy
 comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA

PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX
XX Dislosure; Page 165-172; 268pp; English.
XX
XX The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCNA1, SCNA2 or SCNA3, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCNA1, SCNA2 and SCNA3 are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCNA1, SCNA2 or SCNA3 proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCNA1, SCNA2, and SCNA3 cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
XX
SQ Sequence 1951 AA;

Query Match 100.0%; Score 28; DB 4; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLVFVIFIRFGSFPTLNLFICVIIDNF 28
Db 1395 MYLVFVIFIRFGSFPTLNLFICVIIDNF 1422

RESULT 11
ADES9628
ID ADES9628 standard; protein; 1951 AA.
XX
XX ADES9628;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Proteain NP_037251, SEQ ID NO 5524.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SN1; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI, 2003-268312/26.
XX GENBANK; NP_037251.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1951 AA;

Query Match 100.0%; Score 28; DB 7; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLVFVIFIRFGSFPTLNLFICVIIDNF 28
Db 1395 MYLVFVIFIRFGSFPTLNLFICVIIDNF 1422

RESULT 12
ADL06576
ID ADL06576 standard; protein; 1951 AA.
XX
XX ADL06576;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human tumour-associated antigenic target (TAT) polypeptide #75.
XX
XX Human; tumour-associated antigenic target; TAT; cell death; tumour;
XX cancer; cytostatic.
XX
XX Homo sapiens.
XX
XX WO2004016225-A2.
XX
XX 26-FEB-2004.
XX
XX 19-AUG-2003; 2003WO-US025892.
XX
XX 19-AUG-2002; 2002US-0404809P.
XX PR 21-AUG-2002; 2002US-0405645P.
XX PR 23-SEP-2002; 2002US-0413192P.
XX PR 15-OCT-2002; 2002US-0419008P.
XX PR 15-NOV-2002; 2002US-0426847P.
XX PR 02-JUL-2003; 2003US-0484959P.
XX
XX (GETH) GENENTECH INC.
XX
XX Desauvage FU, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V,
XX Spencer SD, Wu TD, Zhang Z;
XX WPI, 2004-257144/24.
XX N-PSDB; ADL06499.
XX
XX New antibody that binds to a tumor-associated antigenic target (TAT)
XX polypeptide, useful for preparing a composition for diagnosing or

PT treating cancer.
XX
PS Claim 2; SEQ ID NO 156; 319pp; English.
XX
CC The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAT polypeptide of the invention.
XX
SQ Sequence 1951 AA;
XX
Query Match 100.0%; Score 28; DB 8; Length 1951;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MLYLVFVIFIFGSEFTLNLFIGVIIDNF 28
|||
Db 1395 MLYLVFVIFIFGSEFTLNLFIGVIIDNF 1422
XX
RESULT 13
AAE20511
ID AAE20511 standard; protein; 1962 AA.
XX
AC AAE20511;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #2.
XX
DE Human; novel human protein; NHP; voltage-gated sodium channel;
XX gene therapy; bioreactor; mental disorder; biological disorder;
XX medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 981 /note= "Encoded by MTG"
FT Misc-difference 1056 /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI: 2002-280757/32.
DR N-PSDB; AAD32840.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 37-41; 83pp; English.
XX
CC The present sequence is novel human protein (NHP), ion channel protein.
CC NHP share structural similarity with mammalian sodium channel proteins
CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
CC are useful as hybridisation probes for screening libraries and assessing
CC gene expression patterns. Sequences derived from regions adjacent to the

CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
XX
SQ Sequence 1962 AA;
XX
Query Match 100.0%; Score 28; DB 5; Length 1962;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 MLYLVFVIFIFGSEFTLNLFIGVIIDNF 28
|||
Db 1448 MLYLVFVIFIFGSEFTLNLFIGVIIDNF 1475
XX
RESULT 14
AAE20516
ID AAE20516 standard; protein; 1973 AA.
XX
AC AAE20516;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human ion channel protein #7.
XX
DE Human; novel human protein; NHP; voltage-gated sodium channel;
XX gene therapy; bioreactor; mental disorder; biological disorder;
XX medical disorder.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 992 /note= "Encoded by MTG"
FT Misc-difference 1067 /note= "Encoded by RCA"
XX
PN WO200214498-A2.
XX
PD 21-FEB-2002.
XX
PF 15-AUG-2001; 2001WO-US025650.
XX
PR 16-AUG-2000; 2000US-0225989P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Turner CA, Mathur B, Mathur D;
XX
DR WPI: 2002-280757/32.
DR N-PSDB; AAD32845.
XX
PT Novel polynucleotides encoding human sodium channel proteins,
PT particularly voltage-gated sodium channel proteins useful for drug
PT screening, diagnosis and in gene therapy of biological disorders.
XX
PS Claim 1; Page 64-68; 83pp; English.

XX The present sequence is novel human protein (NHP), ion channel protein.
 CC NHP share structural similarity with mammalian sodium channel proteins.
 CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
 CC are useful as hybridisation probes for screening libraries and assessing
 CC gene expression patterns. Sequences derived from regions adjacent to the
 CC intron/exon boundaries of NHP gene can be used to design primers for use
 CC in amplification assays to detect mutations within the exons, splice
 CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
 CC nucleotide sequences are useful for drug screening effective in the
 CC treatment of symptomatic or phenotypic manifestations of perturbing the
 CC normal function of NHP in the body, and nucleotide constructs encoding
 CC NHP products are useful to genetically engineer host cells to express NHP
 CC products in vivo. These genetically engineered cells function as
 CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
 CC peptide, or a NHP fusion protein to the body. Nucleotide construct
 CC encoding NHP products are also useful in gene therapy for modulating NHP
 CC expression and to produce genetically engineered host cells to express
 CC NHP products in vivo. NHP nucleotide sequences may also be used as part
 CC of ribozyme and/or triple helix sequences that are useful for NHP gene
 CC regulation. The NHP polypeptides are useful for generating antibodies, as
 CC reagents in diagnostic assays, for identifying other cellular gene
 CC products related to NHP and as reagents in assays for screening for
 CC compounds that are useful in the treatment of mental, biological or
 CC medical disorders and diseases

SO Sequence 1973 AA;

Query Match 100.0%; Score 28; DB 5; Length 1973;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLYFVFIIFGSPFTLNLFTGVIIDNF 28
 Db 1459 MYLYFVFIIFGSPFTLNLFTGVIIDNF 1486

RESULT 15

ID ABR83185 standard; protein; 1981 AA.

XX ABR83185;

DT 15-JAN-2004 (first entry)

DE Human SCN1A splice variant -84P:SCN1ADELP654-681.

XX SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
 KM neuroprotective; anesthetic; cytoprotective; cerebroprotective; cardiant;
 KW hypotensive; gene therapy; human; splice variant.

OS Homo sapiens.

PN WO2003072751-A2.

PD 04-SEP-2003.

PF 25-FEB-2003; 2003WO-US006010.

PR 25-FEB-2002; 2002US-0359382P.

PA (UVA-) UNIV VANDERBILT.

PI George AL, Loselin C;

DR WPI; 2003-712725/67.

XX N-PSDB; ACF57880.

PT Recombinantly expressed sodium channel type 1 alpha subunit, useful in
 screening for modulators, for treating e.g. epilepsy.

PS Disclosure; Page 162-169; 176pp; English.

CC The invention relates to a recombinantly expressed and isolated human
 CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
 CC incorporated into a cell, is used to screen for specific modulators,
 CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
 CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
 CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
 CC motor endplate diseases, hypertension, congestive heart failure and
 CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
 CC and metastatic cancer cell lines). These activities can also be provided
 CC by gene therapy vectors that express (I) or the modulators. The
 CC modulators, also antibodies directed against (I), are used to detect
 CC sodium channel polypeptides. The present sequence represents a human
 CC SCN1A splice variant 84P:SCN1ADELP654-681

SO Sequence 1981 AA;

Query Match 100.0%; Score 28; DB 7; Length 1981;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLYFVFIIFGSPFTLNLFTGVIIDNF 28
 Db 1431 MYLYFVFIIFGSPFTLNLFTGVIIDNF 1458

RESULT 16

ID AAE20510 standard; protein; 1998 AA.

XX AAE20510;

DT 01-JUL-2002 (first entry)

DE Human ion channel protein #1.

XX Human; novel human protein; NHP; voltage-gated sodium channel;
 KW gene therapy; bioreactor; mental disorder; biological disorder;
 KW medical disorder.

OS Homo sapiens.

PN WO200214498-A2.

PD 21-FEB-2002.

PF 15-AUG-2001; 2001WO-US025650.

PR 16-AUG-2000; 2000US-0225989P.

PA (LEXI-) LEXICON GENETICS INC.

PI Turner CA, Mathur B, Mathur D;

DR WPI; 2002-280757/32.

XX N-PSDB; AAD32839.

PT Novel polynucleotides encoding human sodium channel proteins,
 particularly voltage-gated sodium channel proteins useful for drug
 screening, diagnosis and in gene therapy of biological disorders.

PS Claim 1; Page 30-34; 83pp; English.

XX The present sequence is novel human protein (NHP), ion channel protein.
 CC NHP share structural similarity with mammalian sodium channel proteins
 CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
 CC are useful as hybridisation probes for screening libraries and assessing
 CC gene expression patterns. Sequences derived from regions adjacent to the

CC intron/exon boundaries of NHP gene can be used to design primers for use
CC in amplification assays to detect mutations within the exons, splice
CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
CC nucleotide sequences are useful for drug screening effective in the
CC treatment of symptomatic or phenotypic manifestations of perturbing the
CC normal function of NHP in the body, and nucleotide constructs encoding the
CC NHP products are useful to genetically engineer host cells to express NHP
CC products in vivo. These genetically engineered cells function as
CC bioreactors in the body delivering a continuous supply of a NHP, a NHP
CC peptide, or a NHP fusion protein to the body. Nucleotide construct
CC encoding NHP products are also useful in gene therapy for modulating NHP
CC expression and to produce genetically engineered host cells to express
CC NHP products in vivo. NHP nucleotide sequences may also be used as part
CC of ribozyme and/or triple helix sequences that are useful for NHP gene
CC regulation. The NHP polypeptides are useful for generating antibodies, as
CC reagents in diagnostic assays, for identifying other cellular gene
CC products related to NHP and as reagents in assays for screening for
CC compounds that are useful in the treatment of mental, biological or
CC medical disorders and diseases
CC
SQ Sequence 1998 AA;

Query Match 100.0%; Score 28; DB 5; Length 1998;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLVEVFIIFGSFPTLNLFIGVIIDNF 28
DB 1448 MYLVEVFIIFGSFPTLNLFIGVIIDNF 1475

RESULT 17
ABR83184
ID ABR83184 standard; protein; 1998 AA.

AC ABR83184;
XX
DT 15-JAN-2004 (first entry)
XX

DE Human SCN1A splice variant -33P:SCN1ADELP671-681.
XX

KM SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
KM neuroprotective; anesthetic; cyostatic; cerebroprotective; cardiac;
KM hypotensive; gene therapy; human; splice variant.
XX

OS Homo sapiens.
XX

PN W02003072751-A2.
XX

PD 04-SEP-2003.
XX

PF 25-FEB-2003; 2003WO-US006010.
XX

PR 25-FEB-2002; 2002US-0359382P.
XX

PA (UYVA-) UNIV VANDERBILT.
XX

PI George AL, Lossin C;
XX

DR WPI; 2003-712725/67.
XX

DR N-PSDB; ACF57879.
XX

PT Recombinantly expressed sodium channel type 1 alpha subunit, useful in
screening for modulators, for treating e.g. epilepsy.
XX

PS Disclosure; Page 148-156; 176pp; English.
XX

CC The invention relates to a recombinantly expressed and isolated human
CC SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally
CC incorporated into a cell, is used to screen for specific modulators,
CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,

CC motor endplate diseases, hypertension, congestive heart failure and
CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
CC and metastatic cancer cell lines). These activities can also be provided
CC by gene therapy vectors that express (I) or the modulators. The
CC modulators, also antibodies directed against (I), are used to detect
CC sodium channel polypeptides. The present sequence represents a human
CC SCN1A splice variant 33P:SCN1ADELP671-681 encoding cDNA
XX
SQ Sequence 1998 AA;

Query Match 100.0%; Score 28; DB 7; Length 1998;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLVEVFIIFGSFPTLNLFIGVIIDNF 28
DB 1448 MYLVEVFIIFGSFPTLNLFIGVIIDNF 1475

RESULT 18
ABB06026

ID ABB06026 standard; protein; 1999 AA.
XX

AC ABB06026;
XX

DT 10-MAY-2002 (first entry)
XX

DE Human sodium channel SCN1A protein SEQ ID NO:2.
XX

KM Human; sodium channel; SCN1A; chromosome 2q24;
KM familial hypercalcaemic periodic paralysis; motor endplate disease.
XX

OS Homo sapiens.
XX

PN W0200196552-A1.
XX

PD 20-DEC-2001.
XX

PF 12-JUN-2001; 2001WO-JP004956.
XX

PR 13-JUN-2000; 2000JP-00177540.
XX

PR 13-JUN-2000; 2000JP-00177544.
XX

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX

PI Kanazawa I, Goto J, Jeong S;
XX

DR WPI; 2002-098066/13.
XX

DR N-PSDB; ABL39689.
XX

PT Human sodium channels SCN1A and SCN3A and encoded genes, useful in
studying physiological mechanism in which excitant cells participate and
causes of diseases and developing drugs for motor endplate disease.
XX

PS Claim 1; Page 40-49; 88pp; Japanese.
XX

CC The present invention describes human sodium channels SCN1A and SCN3A.
CC The present sequence represents the human sodium channel SCN1A. SCN3A and
CC SCN3A have been located to the human chromosome 2 long arm, positions
CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
CC studying the physiological mechanism in which excitant cells participate
CC and cause human diseases, and in developing remedies for e.g. familial
CC hypercalcaemic periodic paralysis of extremities and motor endplate
CC disease
XX

SQ Sequence 1999 AA;

Query Match 100.0%; Score 28; DB 5; Length 1998;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLVEVFIIFGSFPTLNLFIGVIIDNF 28
|||||

Db 1449 MYLYFVFIIFGSPFTLNLFIGVIIDNF 1476

RESULT 19

AB06027 standard; protein; 2000 AA.

AC ABB06027;

XX 10-MAY-2002 (first entry)

DT 10-MAY-2002 (first entry)

XX Human sodium channel SCN3A protein SEQ ID NO:4.

DE Human sodium channel SCN3A; chromosome 2q24-31;

KW familial hypercalcaemic periodic paralysis; motor endplate disease.

XX Homo sapiens.

OS WO200196552-A1.

PN 20-DEC-2001.

PD 12-JUN-2001; 2001WO-JP004956.

XX 13-JUN-2000; 2000JP-00177540.

PR 13-JUN-2000; 2000JP-00177544.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA Kanazawa I, Goto J, Jeong S;

PI WPI: 2002-098066/13.

XX N-PSDB; ABL38690.

DR Human sodium channels SCN1A and SCN3A and encoded genes, useful in

PT studying physiological mechanism in which excitant cells participate and

XX causes of diseases and developing drugs for motor endplate disease.

PS Claim 2; Page 72-81; 88pp; Japanese.

XX The present invention describes human sodium channels SCN1A and SCN3A.

CC The present sequence represents the human sodium channel SCN3A. SCN1A and

CC SCN3A have been located to the human chromosome 2 long arm, positions

CC 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in

CC studying the physiological mechanism in which excitant cells participate

CC and cause human diseases, and in developing remedies for e.g. familial

CC hypercalcaemic periodic paralysis of extremities and motor endplate

CC disease

XX Sequence 2000 AA;

SO Query Match 100.0%; Score 28; DB 5; Length 2000;

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLYFVFIIFGSPFTLNLFIGVIIDNF 28

Db 1444 MYLYFVFIIFGSPFTLNLFIGVIIDNF 1471

RESULT 20

ADK81762

ID ADK81762 standard; protein; 2000 AA.

XX ADK81762;

XX 20-MAY-2004 (first entry)

DT 20-MAY-2004 (first entry)

XX Human Nav1.3 protein.

XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;

KW diabetic neuropathy; arthritic pain; migraine headache;

XX infantile epilepsy; ataxia.

XX Homo sapiens.

OS WO2004016754-A2.

PN 26-FEB-2004.

PD 14-AUG-2003; 2003WO-US025465.

XX 14-AUG-2002; 2002US-0403416P.

PR (PANA) PHARMACIA CORP.

XX Roberda SL;

PI WPI: 2004-203785/19.

XX N-PSDB; ADK81761.

DR New antisense compound targeted to a nucleic acid molecule encoding

PT Nav1.3, useful for treating a disease or condition associated

PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure

PT disorder, or ataxia.

XX Disclosure; SEQ ID NO 9096; 417p; English.

XX The present invention relates to an antisense compound targeted to a

CC nucleic acid molecule encoding Nav1.3, where the antisense compound

CC specifically hybridizes with and inhibits the expression of Nav1.3. The

CC compound and composition are useful for treating a disease or condition

CC associated with Nav1.3, e.g. pain including but not limited to

CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,

CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,

CC pain from burns, migraine headache, cluster headache, mild-to-moderate

CC headache; seizure disorder such as childhood seizure disorder, including

CC but not limited to neonatal or infantile epilepsy; or ataxia. The present

CC sequence represents human Nav1.3 protein.

XX Sequence 2000 AA;

SO Query Match 100.0%; Score 28; DB 8; Length 2000;

Best Local Similarity 100.0%; Pred. No. 1.4e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLYFVFIIFGSPFTLNLFIGVIIDNF 28

Db 1444 MYLYFVFIIFGSPFTLNLFIGVIIDNF 1471

RESULT 21

AAB99676

ID AAB99676 standard; protein; 2005 AA.

XX AAB99676;

XX 04-SEP-2001 (first entry)

DT 04-SEP-2001 (first entry)

XX Human adult form of SCN2A protein sequence SEQ ID NO:35.

DE Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;

KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;

XX anticonvulsant; neuroprotective.

XX Homo sapiens.

OS WO200138564-A2.

PN 31-MAY-2001.

PD 24-NOV-2000; 2000WO-CA001404.

XX 26-NOV-1999; 99US-0167623P.

XX (UWMC-) UNIV MCGILL.

XX Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
PI WPI; 2001-355945/37.
XX DR N-PSDB; AAH55793.
XX PT Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.
XX Disclosure; Page 123-130; 268pp; English.
XX The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
SQ Sequence 2005 AA;
Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYLYFVFIIFGSPFTLNLFIGVIIDNF 28
DB 1449 MYLYFVFIIFGSPFTLNLFIGVIIDNF 1476
RESULT 22
AAB99677
ID AAB99677 standard; protein; 2005 AA.
AC AAB99677;
DT 04-SEP-2001 (first entry)
XX Human neonatal form of SCN2A protein sequence SEQ ID NO:36.
XX Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
KW diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
KW anticonvulsant; neuroprotective.
OS Homo sapiens.
XX WO200138564-A2.
XX 31-MAY-2001.
XX 24-NOV-2000; 2000WO-CA001404.
XX 26-NOV-1999; 99US-0167623P.
XX (UYMC-) UNIV MCGILL.
XX Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
PI WPI; 2001-355945/37.
XX DR N-PSDB; AAH55794.
XX Determining a predisposition to epilepsy and/or development of epilepsy
PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
PT variant, equivalent, or mutation which shows a linkage disequilibrium.

XX Disclosure; Page 131-138; 268pp; English.
XX The present invention describes a method (M1) of determining an
CC individual's predisposition to epilepsy and/or development of epilepsy,
CC as well as predicting the individual's response to medication. The method
CC comprises determining the genotype of at least one gene selected from
CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
CC channel genes located on chromosome 2. The idiopathic generalised
CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
CC q31. Compounds identified as modulators of the biological activity of
CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
CC or other neurological disorders. They have anticonvulsant and
CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,
CC oligonucleotides and proteins given in the exemplification of the present
CC invention
SQ Sequence 2005 AA;
Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MYLYFVFIIFGSPFTLNLFIGVIIDNF 28
DB 1449 MYLYFVFIIFGSPFTLNLFIGVIIDNF 1476
RESULT 23
AAB83627
ID AAB83627 standard; protein; 2005 AA.
AC AAB83627;
DT 10-OCT-2002 (first entry)
XX Human GERS+ protein with SCN2A mutation.
XX Human; GERS+; SCN2A; mutant; mutein;
KW generalized epilepsy with febrile seizure plus.
XX Homo sapiens.
XX JP2002136289-A.
XX 14-MAY-2002.
XX 01-NOV-2000; 2000JP-00334969.
XX 01-NOV-2000; 2000JP-00334969.
XX 01-NOV-2000; 2000JP-00334969.
XX (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
XX (RIKA) RIKAGAKU KENKYUSHO.
XX WPI; 2002-552308/59.
XX DR N-PSDB; ABQ79201.
XX A human polynucleotide which is complementary to an mRNA transcribed from
PT a generalized epilepsy with febrile seizure plus (GERS+)-related gene
PT useful for diagnosing GERS+.
XX Claim 10; Page 29-34; 37pp; Japanese.
XX This invention relates to a human polynucleotide which is complementary
CC to an mRNA transcribed from a "generalized epilepsy with febrile seizure
CC plus" (GERS+)-related gene. The gene is useful for diagnosing GERS+. The
CC present sequence represents the human GERS+ protein sequence with SCN2A
CC mutation
SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 5; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1,4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLYFVIRPIFGSFTTLNLFIGVIIDNF 28
1449 MYLYFVIRPIFGSFTTLNLFIGVIIDNF 1476

RESULT 24

ADB78604
ID ADB78604 standard; protein; 2005 AA.

XX ADB78604;

DT 04-DEC-2003 (first entry)

XX Human sodium channel subunit mutant SEQ ID NO:148.

XX murein; mutant; ion channel; ion channel subunit; ICS; nootropic;
XX neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
XX antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;
XX nephrotoxic; antidiabetic; ophthalmological; epilepsy;
XX ion channel dysfunction; human.

XX Synthetic.

OS Homo sapiens.

XX WO2003008574-A1.

XX 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.

XX 18-JUL-2001; 2001AU-00006452.

XX 05-MAR-2002; 2002AU-00000910.

XX 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

XX (WALL/) WALLACE R W.

XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

XX Berkovic SF, Scheffer IE;

XX WPI; 2003-239332/23.

XX N-PSDB; ADB78643.

XX Claim 13; SEQ ID NO 148; 106pp; English.

XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has nootropic, neuroprotective, inotropic, antipyretic,
XX antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
XX neuroleptic, tranquilizer, analgesic, nephrotoxic, antidiabetic, and
XX ophthalmological activity. A polynucleotide of the invention acts as an
XX ion channel agonist, or ion channel antagonist. The methods, isolated
XX nucleic acids, polypeptides, antibody, selective agonist, antagonist or
XX modulator of an ion channel, cells and genetically modified non-human
XX animal, are useful for the diagnosis and treatment of epilepsy and/or a
XX disorder associated with ion channel dysfunction, such as hyper- or hypo-
XX kalemia periodic paralysis, myotonia, malignant hyperthermia,
XX myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
XX disease, Parkinson's disease, schizophrenia, hyperplexia, anxiety,
XX depression, phobic obsessive symptoms, neuropathic pain, inflammatory
XX pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,

CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 2005 AA;

QY 1 MYLYFVIRPIFGSFTTLNLFIGVIIDNF 28
1449 MYLYFVIRPIFGSFTTLNLFIGVIIDNF 1476

Db 1449 MYLYFVIRPIFGSFTTLNLFIGVIIDNF 1476

RESULT 25

ADB78603
ID ADB78603 standard; protein; 2005 AA.

XX ADB78603;

DT 04-DEC-2003 (first entry)

XX Human sodium channel subunit mutant SEQ ID NO:147.

XX murein; mutant; ion channel; ion channel subunit; ICS; nootropic;
XX neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;
XX antidepressant; antiparkinsonian; neuroleptic; tranquilizer; analgesic;
XX nephrotoxic; antidiabetic; ophthalmological; epilepsy;
XX ion channel dysfunction; human.

XX Synthetic.

OS Homo sapiens.

XX WO2003008574-A1.

XX 30-JAN-2003.

XX 08-JUL-2002; 2002WO-AU000910.

XX 18-JUL-2001; 2001AU-00006452.

XX 05-MAR-2002; 2002AU-00000910.

XX 13-MAY-2002; 2002AU-00002292.

XX (BION-) BIONOMICS LTD.

XX (WALL/) WALLACE R W.

XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;

XX Berkovic SF, Scheffer IE;

XX WPI; 2003-239332/23.

XX N-PSDB; ADB78642.

XX Claim 13; SEQ ID NO 147; 106pp; English.

XX The invention relates to a novel method for identifying a subject
XX predisposed to a disorder associated with ion channel dysfunction. The
XX method comprises ascertaining if at least one of the genes encoding ion
XX channel subunits (ICS) has undergone a mutation event so that a cDNA
XX derived from the subject has any of 134 nucleotide sequences. The method
XX of the invention has nootropic, neuroprotective, inotropic, antipyretic,
XX antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
XX neuroleptic, tranquilizer, analgesic, nephrotoxic, antidiabetic, and
XX ophthalmological activity. A polynucleotide of the invention acts as an
XX ion channel agonist, or ion channel antagonist. The methods, isolated

CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
 CC modulator of an ion channel, cells and genetically modified non-human
 CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
 CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
 CC kalemic periodic paralysis, myotonia, malignant hyperthermia,
 CC myasthenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
 CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
 CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
 CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
 CC fibrosis, congenital stationary night blindness and total colour
 CC blindness. The present sequence represents a mutant protein of the
 CC invention. The sequence data for this patent is not represented in the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at [ftp.wipo.int/pub/published_pat_sequences](http://wipo.int/pub/published_pat_sequences).
 XX

Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 7; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MYLYFVIFIIIPGSPFTLNLFIVGIIDNF 28
 |||||
 Db 1449 MYLYFVIFIIIPGSPFTLNLFIVGIIDNF 1476

Search completed: January 27, 2005, 17:45:16
 Job time : 87.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:05 ; Search time 17 Seconds
(without alignments)
158.475 Million cell updates/sec

Title: US-10-608-584-19

Perfect score: 28
Sequence: 1 MVLVYFIFIFGSPFTLNLFGVINDNF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : PIR_79:**

1: p1r1:**
2: p1r2:**
3: p1r3:**
4: p1r4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	1835	2	154333
2	28	100.0	1836	2	164893
3	28	100.0	1836	2	150648
4	28	100.0	1836	2	151964
5	28	100.0	1840	1	CHRTM1
6	28	100.0	1951	2	S00320
7	28	100.0	1983	2	A60054
8	28	100.0	2005	2	A46269
9	28	100.0	2005	2	B25019
10	28	100.0	2009	2	A25019
11	25	89.3	1976	2	I56555
12	25	89.3	2016	2	A38195
13	21	75.0	2295	2	A56595
14	21	75.0	1689	2	S72467
15	21	75.0	1699	2	T31340
16	21	75.0	1765	2	T42388
17	21	75.0	1784	2	T43167
18	21	75.0	1820	2	A33289
19	21	75.0	1977	2	S54771
20	21	75.0	2019	2	A53996
21	21	75.0	2108	2	S72458
22	18	64.3	2049	2	T43161
23	17	60.7	1321	2	A60165
24	17	60.7	1810	2	T31092
25	15	53.6	1820	1	CHER
26	13	46.4	1993	2	T30902
27	12	42.9	1695	2	J60084
28	12	42.9	1739	2	A48298
29	8	28.6	1522	2	JC1101

30	7	25.0	260	2	G81290	probable capsule p
31	7	25.0	274	2	E83837	hypothetical prote
32	7	25.0	351	2	A69808	H+/Ca2+ exchanger
33	7	25.0	399	2	E84964	hypothetical prote
34	7	25.0	491	2	T73524	hypothetical prote
35	7	25.0	494	1	O4H0A6	coumarin-7-hydroxy
36	7	25.0	542	2	E90457	hypothetical prote
37	7	25.0	568453	2	S68453	sodium channel pro
38	22	21.4	1957	2	S17303	tegumental glycop
39	6	21.4	22	2	C90105	60S ribosomal prot
40	6	21.4	118	2	C90105	hypothetical prote
41	6	21.4	129	2	T75141	hypothetical prote
42	6	21.4	130	2	C90503	conserved hypothet
43	6	21.4	153	2	S52605	probable membrane
44	6	21.4	155	2	A91055	hypothetical prote
45	6	21.4	155	2	D85899	hypothetical prote
46	6	21.4	162	2	T13574	MADH2 dehydrogenas
47	6	21.4	164	2	E65031	hypothetical prote
48	6	21.4	164	2	H71175	hypothetical prote
49	6	21.4	182	1	RSMX6	ribosomal protein
50	6	21.4	182	2	A45553	22K surface membra
51	6	21.4	184	2	B90592	hypothetical prote
52	6	21.4	192	2	S09506	hypothetical prote
53	6	21.4	218	2	S43591	W04D8.4 protein
54	6	21.4	220	2	B64681	nicotinamide monon
55	6	21.4	220	2	B71832	hypothetical prote
56	6	21.4	221	2	D86878	hypothetical prote
57	6	21.4	237	2	S64315	hypothetical prote
58	6	21.4	240	2	H84457	probable replicati
59	6	21.4	248	2	S57461	H+-transporting tw
60	6	21.4	251	2	S38811	hypothetical prote
61	6	21.4	254	2	E97242	signal peptidase t
62	6	21.4	256	2	AG0413	probable ABC trans
63	6	21.4	258	2	E72319	flagellar biosynth
64	6	21.4	259	2	A83284	probable permease
65	6	21.4	261	2	AD1721	hypothetical prote
66	6	21.4	261	2	E90506	hypothetical prote
67	6	21.4	279	2	E70332	hypothetical prote
68	6	21.4	282	2	C84114	UDP-glucose 4-epim
69	6	21.4	286	2	I46855	voltage-gated pola
70	6	21.4	314	2	T32672	hypothetical prote
71	6	21.4	316	2	S46055	probable membrane
72	6	21.4	317	2	A71698	hypothetical prote
73	6	21.4	322	2	E81279	enterochelin uptak
74	6	21.4	322	2	D96921	oligopeptide trans
75	6	21.4	331	1	O4H0B3	cytochrome P450 2A
76	6	21.4	333	2	B84195	hypothetical prote
77	6	21.4	335	2	G83598	cell division prot
78	6	21.4	336	2	F75320	WD-repeat family P
79	6	21.4	339	2	S61020	probable membrane
80	6	21.4	340	2	S41752	UDP-3-O-[3-hydroxy
81	6	21.4	340	2	A60129	UDP-3-O-[3-hydroxy
82	6	21.4	341	2	AD0530	UDP-3-O-[3-hydroxy
83	6	21.4	341	2	S13729	UDP-3-O-[3-hydroxy
84	6	21.4	341	2	E85502	hypothetical prote
85	6	21.4	341	2	E90651	hypothetical prote
86	6	21.4	341	2	B37083	Sac protein - Salm
87	6	21.4	345	2	T12354	MADH2 dehydrogenas
88	6	21.4	351	2	E97768	microcin C7 self-i
89	6	21.4	365	2	A63119	hypothetical prote
90	6	21.4	374	2	A98168	hypothetical prote
91	6	21.4	375	2	D82894	heat shock protein
92	6	21.4	381	2	S59093	ubiquinol-cytochro
93	6	21.4	390	2	D75093	macrolide-efflux d
94	6	21.4	406	2	T23934	hypothetical prote
95	6	21.4	409	2	AG0235	probable sugar tra
96	6	21.4	409	2	T47026	hypothetical prote
97	6	21.4	411	2	E84949	tetrahydrofolylpol
98	6	21.4	434	2	AH1990	hypothetical prote
99	6	21.4	437	2	G82777	glutamate symport
100	6	21.4	444	2	F71916	probable lipopolys
	6	21.4	468	2	S75389	probable phenylala

ALIGNMENTS

RESULT 1

154323
sodium channel alpha subunit - human
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C/Accession: 154323
R/McClatchey, A.I.; Lin, C.S.; Wang, J.; Hoffman, E.P.; Rojas, C.; Gussella, J.F.
Hum. Mol. Genet. 1, 521-527, 1992
A/Title: The genomic structure of the human skeletal muscle sodium channel gene.
A/Accession number: 154323, MUID:9338444, PMID:1339144
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-1835 <RES>
A/Cross-references: GB:I01983; NID:9337992; PIDN:AAA75557.1; PID:9908809
C/Genetics:
A/Gene: GDB:SCN4A
A/Cross-references: GDB:125181; OMIM:170500
A/Map position: 17q23.1-17q25.3
A/Insertions: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3;
C/Superfamily: sodium channel protein
C/Keywords: duplication

Query Match 100.0%; Score 28; DB 2; Length 1835;
Best Local Similarity 100.0%; Pred. No. 3,4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MYLYFVFIIFGSPFTLNLFQVITDNF 28
1271 MYLYFVFIIFGSPFTLNLFQVITDNF 1298

RESULT 2

164893
sodium channel alpha subunit - human
C/Species: Homo sapiens (man)
C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C/Accession: 164893
R/George, A.L.
Ann. Neurol. 31, 131-137, 1992
A/Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium c
A/Reference number: 151964, MUID:92246457, PMID:1315496
A/Accession: 164893
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-1836 <RES>
A/Cross-references: UNIPROT:P35499; GB:M81758; NID:9338212; PIDN:AAA60554.1; PID:9338213
C/Genetics:
A/Gene: SKM1
C/Superfamily: sodium channel protein
C/Keywords: duplication

Query Match 100.0%; Score 28; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 3,4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MYLYFVFIIFGSPFTLNLFQVITDNF 28
1271 MYLYFVFIIFGSPFTLNLFQVITDNF 1298

RESULT 3

JS0648
sodium channel alpha chain - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: JS0648, A42099
R/Wang, J.; Rojas, C.V.; Zhou, J.; Schwartz, L.S.; Nicholas, H.; Hoffmann, E.P.
Biochem. Biophys. Res. Commun. 182, 794-801, 1992
A/Title: Sequence and genomic structure of the human adult skeletal muscle sodium channel

A/Reference number: JS0648; MUID:92134303; PMID:1310396
A/Accession: JS0648
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1836 <MAN>

A/Cross-references: UNIPROT:P35499
A/Note: 861-Asp was also found as the result of polymorphism
R/McClatchey, A.I.; Van den Bergh, P.; Pericak-Vance, M.A.; Raekind, W.; Verellen, C.; Mc
Cell 68, 769-774, 1992

A/Title: Temperature-sensitive mutations in the III-IV cytoplasmic loop region of the s
A/Reference number: A42099; MUID:92154689; PMID:1310898
A/Accession: A42099

A/Molecule type: DNA

A/Residues: 1299-1351 <MCC>

A/Cross-references: GB:S82622; NID:9245611; PIDN:AAB21450.1; PID:9245612

A/Experimental source: skeletal muscle
A/Note: sequence extracted from NCBI backbone (NCBIN:82622, NCBIP:82623)

C/Genetics:
A/Gene: GDB:SCN4A

A/Cross-references: GDB:125181; OMIM:170500
A/Map position: 17q23.1-17q25.3

C/Superfamily: sodium channel protein
C/Keywords: duplication; glycoprotein; phosphoprotein; transmembrane protein

F:129-150/Domain: transmembrane #status predicted <R1>
F:159-178/Domain: transmembrane #status predicted <R1>
F:191-210/Domain: transmembrane #status predicted <R2>
F:211-236/Domain: transmembrane #status predicted <R3>
F:251-266/Domain: transmembrane #status predicted <R4>
F:284-299/Domain: transmembrane #status predicted <R5>
F:324-349/Domain: transmembrane #status predicted <R6>
F:354-379/Domain: transmembrane #status predicted <R7>
F:409-434/Domain: transmembrane #status predicted <R8>
F:444-469/Domain: transmembrane #status predicted <R9>
F:494-519/Domain: transmembrane #status predicted <R10>
F:544-569/Domain: transmembrane #status predicted <R11>
F:594-619/Domain: transmembrane #status predicted <R12>
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F:694-719/Domain: transmembrane #status predicted <R14>
F:744-769/Domain: transmembrane #status predicted <R15>
F:794-819/Domain: transmembrane #status predicted <R16>
F:844-869/Domain: transmembrane #status predicted <R17>
F:894-919/Domain: transmembrane #status predicted <R18>
F:944-969/Domain: transmembrane #status predicted <R19>
F:1004-1029/Domain: transmembrane #status predicted <R20>
F:1054-1079/Domain: transmembrane #status predicted <R21>
F:1104-1129/Domain: transmembrane #status predicted <R22>
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F:1254-1279/Domain: transmembrane #status predicted <R25>
F:1304-1329/Domain: transmembrane #status predicted <R26>
F:1354-1379/Domain: transmembrane #status predicted <R27>
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F:1854-1879/Domain: transmembrane #status predicted <R37>
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F:1954-1979/Domain: transmembrane #status predicted <R39>
F:2004-2029/Domain: transmembrane #status predicted <R40>
F:2054-2079/Domain: transmembrane #status predicted <R41>
F:2104-2129/Domain: transmembrane #status predicted <R42>
F:2154-2179/Domain: transmembrane #status predicted <R43>
F:2204-2229/Domain: transmembrane #status predicted <R44>
F:2254-2279/Domain: transmembrane #status predicted <R45>
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F:2354-2379/Domain: transmembrane #status predicted <R47>
F:2404-2429/Domain: transmembrane #status predicted <R48>
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F:2654-2679/Domain: transmembrane #status predicted <R53>
F:2704-2729/Domain: transmembrane #status predicted <R54>
F:2754-2779/Domain: transmembrane #status predicted <R55>
F:2804-2829/Domain: transmembrane #status predicted <R56>
F:2854-2879/Domain: transmembrane #status predicted <R57>
F:2904-2929/Domain: transmembrane #status predicted <R58>
F:2954-2979/Domain: transmembrane #status predicted <R59>
F:3004-3029/Domain: transmembrane #status predicted <R60>
F:3054-3079/Domain: transmembrane #status predicted <R61>
F:3104-3129/Domain: transmembrane #status predicted <R62>
F:3154-3179/Domain: transmembrane #status predicted <R63>
F:3204-3229/Domain: transmembrane #status predicted <R64>
F:3254-3279/Domain: transmembrane #status predicted <R65>
F:3304-3329/Domain: transmembrane #status predicted <R66>
F:3354-3379/Domain: transmembrane #status predicted <R67>
F:3404-3429/Domain: transmembrane #status predicted <R68>
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F:3604-3629/Domain: transmembrane #status predicted <R72>
F:3654-3679/Domain: transmembrane #status predicted <R73>
F:3704-3729/Domain: transmembrane #status predicted <R74>
F:3754-3779/Domain: transmembrane #status predicted <R75>
F:3804-3829/Domain: transmembrane #status predicted <R76>
F:3854-3879/Domain: transmembrane #status predicted <R77>
F:3904-3929/Domain: transmembrane #status predicted <R78>
F:3954-3979/Domain: transmembrane #status predicted <R79>
F:4004-4029/Domain: transmembrane #status predicted <R80>
F:4054-4079/Domain: transmembrane #status predicted <R81>
F:4104-4129/Domain: transmembrane #status predicted <R82>
F:4154-4179/Domain: transmembrane #status predicted <R83>
F:4204-4229/Domain: transmembrane #status predicted <R84>
F:4254-4279/Domain: transmembrane #status predicted <R85>
F:4304-4329/Domain: transmembrane #status predicted <R86>
F:4354-4379/Domain: transmembrane #status predicted <R87>
F:4404-4429/Domain: transmembrane #status predicted <R88>
F:4454-4479/Domain: transmembrane #status predicted <R89>
F:4504-4529/Domain: transmembrane #status predicted <R90>
F:4554-4579/Domain: transmembrane #status predicted <R91>
F:4604-4629/Domain: transmembrane #status predicted <R92>
F:4654-4679/Domain: transmembrane #status predicted <R93>
F:4704-4729/Domain: transmembrane #status predicted <R94>
F:4754-4779/Domain: transmembrane #status predicted <R95>
F:4804-4829/Domain: transmembrane #status predicted <R96>
F:4854-4879/Domain: transmembrane #status predicted <R97>
F:4904-4929/Domain: transmembrane #status predicted <R98>
F:4954-4979/Domain: transmembrane #status predicted <R99>
F:5004-5029/Domain: transmembrane #status predicted <R100>

Query Match 100.0%; Score 28; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 3,4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MYLYFVFIIFGSPFTLNLFQVITDNF 28
1271 MYLYFVFIIFGSPFTLNLFQVITDNF 1298

RESULT 4

151964
sodium channel alpha chain SCN4A, skeletal muscle - human
C/Species: Homo sapiens (man)
C/Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C/Accession: 151964
R/George, A.L.
Ann. Neurol. 31, 131-137, 1992
A/Title: Primary structure of the adult human skeletal muscle voltage-dependent sodium c
A/Reference number: 151964, MUID:92246457, PMID:1315496
A/Accession: 151964

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1836 <RES>
A:Cross-references: UNIPROT:P35499; GB:L04236; NID:G292485; PIDN:AAB59624.1; PID:G292487
C:Genetics:
A:Gene: GDB:SCN4A
A:Cross-references: GDB:125181; OMIM:170500
A:Map position: 17q23.1-17q25.3
A:Insertions: 91/3; 131/2; 161/2; 204/2; 235/1; 346/1; 367/2; 414/3; 484/3; 536/1; 615/3; 6
C:Superfamily: sodium channel protein
C:Keywords: duplication; skeletal muscle

Query Match 100.0%; Score 28; DB 2; Length 1836;
Best Local Similarity 100.0%; Pred. No. 3.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MYLFFVFIIFGSPFTLNLFGVIIDNF 28
Db 1271 MYLFFVFIIFGSPFTLNLFGVIIDNF 1298

RESULT 5
CHRTM1
sodium channel protein mu1 alpha chain, skeletal muscle - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C:Accession: JN0007
R:Trimmer, J.S.; Cooperman, S.S.; Tomiko, S.A.; Zhou, J.; Crean, S.M.; Boyle, M.B.; Kall
Neuron 3, 33-49, 1989
A:Title: Primary structure and functional expression of a mammalian skeletal muscle sodi
A:Reference number: JN0007; MUID:90148778; PMID:2559760
A:Accession: JN0007
A:Molecule type: mRNA
A:Residues: 1-1840 <TRI>
A:Cross-references: UNIPROT:P15390; GB:M26643; NID:G205651; PIDN:AAA41682.1; PID:G205652
C:Comment: Action potentials propagated by skeletal muscle sodium channels are responsib
C:Comment: This heavily glycosylated protein contains four homologous domains, each of w
C:Comment: This protein is distinct from but related to sodium channel proteins isolated
C:Superfamily: sodium channel protein
C:Keywords: duplication; glycoprotein; ion transport; neuromuscular junction; phosphoprc
F:120-458,561-813,1013-1305,1335-1611,Region: duplication
F:56,251,1321,1504/Binding site: phosphatase (Ser) (covalent) (by CAMP-dependent kinase) #
F:214,288,291,297,309,315,327,356,502,696,954,1184,1198,1563,1702/Binding site: catr

Query Match 100.0%; Score 28; DB 1; Length 1840;
Best Local Similarity 100.0%; Pred. No. 3.4e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MYLFFVFIIFGSPFTLNLFGVIIDNF 28
Db 1264 MYLFFVFIIFGSPFTLNLFGVIIDNF 1291

RESULT 6
S00320
sodium channel protein III - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: S00320
R:Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S.
FEBS Lett. 228, 187-194, 1988
A:Title: Primary structure of rat brain sodium channel III deduced from the cDNA sequenc
A:Reference number: S00320; MUID:88137594; PMID:2449363
A:Accession: S00320
A:Molecule type: mRNA
A:Residues: 1-1951 <RAY>
A:Cross-references: UNIPROT:P08104; EMBL:X00766; NID:G57210; PIDN:CA68735.1; PID:G57211
A:Note: 270-Ile, 278-Ileu, 355-Lys, 513-Lys, and 1059-Arg were also found
C:Superfamily: sodium channel protein
C:Keywords: duplication; transmembrane protein

Query Match 100.0%; Score 28; DB 2; Length 1951;
Best Local Similarity 100.0%; Pred. No. 3.6e-20;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MYLFFVFIIFGSPFTLNLFGVIIDNF 28
Db 1395 MYLFFVFIIFGSPFTLNLFGVIIDNF 1422

RESULT 7
A60054
sodium channel protein IIB, long form - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: A60054; B44824
R:Joho, R.H.; Moorman, J.R.; Vandongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster, B
Brain Res. Mol. Brain Res. 7, 105-113, 1990
A:Title: Toxin and kinetic profile of rat brain type IIB sodium channels expressed in Xe
A:Reference number: A60054; MUID:90251117; PMID:2160038
A:Accession: A60054
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1983 <JOH>
A:Cross-references: UNIPROT:Q64243
R:Schaller, K.U.; Krzemien, D.M.; McKenna, N.M.; Caldwell, J.H.
J. Neurosci. 12, 1370-1381, 1992
A:Title: Alternatively spliced sodium channel transcripts in brain and muscle.
A:Reference number: A44824; MUID:92211397; PMID:1313493
A:Accession: B44824
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 611-662 <SCH>
A:Cross-references: GB:S97388; NID:G248225; PIDN:AAB21984.1; PID:G248226
A:Experimental source: skeletal muscle
A:Note: sequence inconsistent with the nucleotide translation
C:Superfamily: sodium channel protein
C:Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane prot

Query Match 100.0%; Score 28; DB 2; Length 1983;
Best Local Similarity 100.0%; Pred. No. 3.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MYLFFVFIIFGSPFTLNLFGVIIDNF 28
Db 1427 MYLFFVFIIFGSPFTLNLFGVIIDNF 1454

RESULT 8
A46269
sodium channel alpha chain HBA - human
C:Species: Homo sapiens (man)
C>Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
C:Accession: A46269
R:Almed, C.M.; Ware, D.H.; Lee, S.C.; Patten, C.D.; Ferrer-Montiel, A.V.; Schindler, A.F.
Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992
A:Title: Primary structure, chromosomal localization, and functional expression of a vol
A:Reference number: A46269; MUID:92390418; PMID:11355650
A:Accession: A46269
A:Molecule type: mRNA
A:Residues: 1-2005 <AHM>
A:Cross-references: GB:M94055
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBI:P113082)
C:Genetics:
A:Map position: 2q23-q24.3
C:Superfamily: sodium channel protein
C:Keywords: duplication

Query Match 100.0%; Score 28; DB 2; Length 2005;
Best Local Similarity 100.0%; Pred. No. 3.7e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MYLFFVFIIFGSPFTLNLFGVIIDNF 28

Db 1449 MYLFFVFIIFGSEFTLNLFIVIIDNF 1476

RESULT 9

B25019

sodium channel protein II - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1988 #sequence _revision 30-Jun-1988 #text_change 09-Jul-2004

C/Accession: B25019; S24804

R/Node: M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H.

A/Title: Existence of distinct sodium channel messenger RNAs in rat brain.

A/Reference number: A93377; MUID:86146901; PMID:3754035

A/Accession: B25019

A/Molecule type: mRNA

A/Residues: 1-2005 <NOD>

A/Cross-references: UNIPROT:Q63509

A/Experimental source: brain

R/Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.

Submitted to the EMBL Data Library, August 1991.

A/Description: Developmentally regulated RNA splicing of rat brain sodium channel mRNAs.

A/Reference number: S24804

A/Accession: S24804

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 183-188, 'D', 190-305 <SAR>

A/Cross-references: EMBL:X61149; NID:957074; PIDN:CAA43458.1; PID:957076

C/Superfamily: sodium channel protein

C/Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 2005;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLFFVFIIFGSEFTLNLFIVIIDNF 28

Db 1449 MYLFFVFIIFGSEFTLNLFIVIIDNF 1476

RESULT 10

A25019

sodium channel protein I - rat

N/Alternate names: sodium channel protein A

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1988 #sequence _revision 30-Jun-1988 #text_change 09-Jul-2004

C/Accession: A25019; S40783; T84764

R/Node: M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H.

A/Title: Existence of distinct sodium channel messenger RNAs in rat brain.

A/Reference number: A93377; MUID:86146901; PMID:3754035

A/Accession: A25019

A/Molecule type: mRNA

A/Residues: 1-2009 <NOD>

A/Cross-references: UNIPROT:P04774; GB:X03638; NID:957216; PIDN:CAA27286.1; PID:957217

A/Experimental source: brain

R/Sarao, R.; Gupta, S.K.; Auld, V.J.; Dunn, R.J.

Submitted to the EMBL Data Library, August 1991.

A/Description: Developmentally regulated alternative RNA splicing of rat brain sodium channel

A/Reference number: S40783; MUID:92051314; PMID:1658739

A/Accession: S40783

A/Molecule type: DNA

A/Residues: 177-253 <SAR>

R/Node: M.; Numa, S.

J. Recept. Res. 7, 467-497, 1987

A/Title: Structure and function of sodium channel.

A/Reference number: 150536; MUID:87311395; PMID:2442385

A/Accession: 184764

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-2009 <RES>

C/Superfamily: sodium channel protein

C/Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 2009;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLFFVFIIFGSEFTLNLFIVIIDNF 28

Db 1459 MYLFFVFIIFGSEFTLNLFIVIIDNF 1486

RESULT 11

I56555

sodium channel protein 6 - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 26-Jul-1996 #sequence _revision 26-Jul-1996 #text_change 09-Jul-2004

C/Accession: I56555

R/Schaller, K.L.; Krzemien, D.M.; Yarowsky, P.J.; Krueger, B.K.; Caldwell, J.H.

J. Neurosci. 15, 3231-3242, 1995

A/Title: A novel, abundant sodium channel expressed in neurons and glia.

A/Reference number: I56555; MUID:95271284; PMID:7751906

A/Accession: I56555

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1976 <RES>

A/Cross-references: UNIPROT:Q63541; GB:I39018; NID:9829033; PIDN:AA42059.1; PID:9829034

C/Superfamily: sodium channel protein

C/Keywords: duplication

Query Match

Best Local Similarity 89.3%; Score 25; DB 2; Length 1976;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVFIIFGSEFTLNLFIVIIDNF 28

Db 1439 YFVFIIFGSEFTLNLFIVIIDNF 1463

RESULT 12

A38195

sodium channel protein hH1, cardiac - human

N/Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-I Nat

C/Species: Homo sapiens (man)

C/Date: 31-Dec-1993 #sequence _revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: A38195

R/Gellens, M.E.; George Jr., A.L.; Chen, L.O.; Chahine, M.; Horn, R.; Barchi, R.L.; Kall

Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992

A/Title: Primary structure and functional expression of the human cardiac tetrodotoxin-I

A/Reference number: A38195; MUID:92115699; PMID:1309946

A/Accession: A38195

A/Molecule type: mRNA

A/Residues: 1-2016 <GEL>

A/Cross-references: UNIPROT:Q14524; GB:M77235; NID:9184038; PIDN:AA58644.1; PID:9184039

A/Experimental source: heart

C/Superfamily: sodium channel protein

C/Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium chan

Query Match

Best Local Similarity 89.3%; Score 25; DB 2; Length 2016;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVFIIFGSEFTLNLFIVIIDNF 28

Db 1449 YFVFIIFGSEFTLNLFIVIIDNF 1473

RESULT 13

A56595

sodium channel alpha chain hscp - tobacco budworm (fragment)

C/Species: Heliothis virescens (tobacco budworm)

C/Date: 11-Aug-1995 #sequence _revision 11-Aug-1995 #text_change 09-Jul-2004

C/Accession: A56595
 R/Taylor, M.F.; Heckel, D.G.; Brown, T.M.; Kretzman, M.E.; Black, B.
 Insect Biochem. Mol. Biol. 23, 763-775, 1993
 A/Title: Linkage of pyrethroid insecticide resistance to a sodium channel locus in the t
 A/Reference number: A56595; MUID:93386183; PMID:8397035
 A/Accession: A56595
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-295 <TAY>
 A/Cross-references: UNIPROT:Q25178; GB:U24236
 A/Experimental source: pyrethroid resistant strain PEG-87
 A/Note: authors translated the codons GGC for residue 122 as Ala, GTA for residue 238 as
 C/Superfamily: sodium channel protein
 C/Keywords: duplication

Query Match 75.0%; Score 21; DB 2; Length 295;
 Best Local Similarity 100.0%; Pred. No. 7.2e-14;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 FIIFGSFPTNLFIGVIIDNF 28
 Db 94 FIIFGSFPTNLFIGVIIDNF 114

RESULT 14
 S72467
 sodium channel protein para-type alpha chain - German cockroach (strain CSMA) (fragment)
 C/Species: Blattella germanica (German cockroach)
 A/Variety: strain CSMA
 C/Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
 C/Accession: S72467; S72487
 R/Miyazaki, M.; Ohyama, K.; Dunlap, D.Y.; Matsunura, F.
 submitted to the EMBL Data Library, September 1996
 A/Description: Cloning and sequencing of the para-type sodium channel gene from suscepti
 A/Reference number: S72467
 A/Accession: S72467
 A/Molecule type: mRNA
 A/Residues: 1-1689 <MY>
 A/Cross-references: UNIPROT:Q93135; EMBL:U71083; NID:g1633647; PIDN:AB82037.1; PID:g163

Mol. Gen. Genet. 252, 61-68, 1996
 A/Title: Cloning and sequencing of the para-type sodium channel gene from susceptible ar
 A/Reference number: S72487; MUID:96397510; PMID:8804404
 A/Accession: S72487
 A/Molecule type: mRNA
 A/Residues: 711-819 <MY>
 A/Cross-references: EMBL:U71083
 C/Superfamily: sodium channel protein
 C/Keywords: duplication; sodium channel; transmembrane protein

Query Match 75.0%; Score 21; DB 2; Length 1689;
 Best Local Similarity 100.0%; Pred. No. 3.3e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 FIIFGSFPTNLFIGVIIDNF 28
 Db 1304 FIIFGSFPTNLFIGVIIDNF 1324

RESULT 15
 T31340
 voltage-gated sodium channel homolog - Bdelioura candida

C/Species: Bdelioura candida
 C/Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
 C/Accession: T31340
 R/Jezioriski, M.C.; Greenberg, R.M.; Anderson, P.A.
 submitted to the EMBL Data Library, March 1997
 A/Description: A putative voltage-gated sodium channel from the turbellarian flatworm Bd

A/Reference number: Z21006
 A/Accession: T31340
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1699 <JEZ>

A/Cross-references: UNIPROT:O02037; EMBL:U93074; NID:g1947093; PID:g1947094; PIDN:AAC630
 C/Genetics:
 A/Gene: Na1
 C/Superfamily: sodium channel protein

Query Match 75.0%; Score 21; DB 2; Length 1699;
 Best Local Similarity 100.0%; Pred. No. 3.3e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 FIIFGSFPTNLFIGVIIDNF 28
 Db 1231 FIIFGSFPTNLFIGVIIDNF 1251

RESULT 16
 T42388
 sodium channel alpha chain - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C/Accession: T42388
 R/Db-Hajj, S.D.; Tyrrell, L.; Black, J.A.; Waxman, S.G.
 Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998
 A/Title: Na^v1.4, a novel voltage-gated Na channel, is expressed preferentially in periphera
 A/Reference number: Z22149; MUID:98338024; PMID:9671787
 A/Accession: T42388
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-1765 <DIB>
 A/Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC4
 A/Experimental source: strain Sprague-Dawley; dorsal root ganglia
 A/Note: preferentially expressed in sensory neurons within dorsal root ganglia and trigem
 C/Superfamily: sodium channel protein

Query Match 75.0%; Score 21; DB 2; Length 1765;
 Best Local Similarity 100.0%; Pred. No. 3.4e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 FIIFGSFPTNLFIGVIIDNF 28
 Db 1271 FIIFGSFPTNLFIGVIIDNF 1291

RESULT 17
 T43167
 sodium channel protein - California market squid
 C/Species: Loligo opalescens (California market squid)
 C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
 C/Accession: T43167
 R/Rosenthal, J.J.; Gilly, W.F.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10026-10030, 1993
 A/Title: Amino acid sequence of a putative sodium channel expressed in the giant axon of

A/Reference number: Z22324; MUID:94052096; PMID:8234251
 A/Accession: T43167
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Residues: 1-1784 <ROS>
 A/Cross-references: UNIPROT:Q25377; EMBL:L19979; NID:g349118; PID:g349119; PIDN:AAA16202
 A/Experimental source: stellate ganglia
 C/Superfamily: sodium channel protein
 C/Keywords: ion transport; membrane protein; sodium channel; voltage-gated ion channel

Query Match 75.0%; Score 21; DB 2; Length 1784;
 Best Local Similarity 100.0%; Pred. No. 3.4e-13;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 FIIFGSFPTNLFIGVIIDNF 28
 Db 1268 FIIFGSFPTNLFIGVIIDNF 1288

RESULT 18
 A33299
 sodium channel protein - fruit fly (Drosophila melanogaster) (fragment)

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C/Species: Drosophila melanogaster
C/Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 21-Nov-1997
C/Accession: A33299
R/Loughney, K.; Kreber, R.; Ganetzky, B.
Cell 58, 1143-1154, 1989
A/Title: Molecular analysis of the para locus, a sodium channel gene in Drosophila.
A/Reference number: A33299; MUID:89376565; PMID:2550145
A/Accession: A33299
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1820 <IDU>
A/Cross-references: GB:M2078; GB:M24285
C/Genetics:
A/Gene: FlyBase:para
A/Cross-references: FlyBase:FBgn0003036
C/Superfamily: sodium channel protein
C/Keywords: duplication; phosphoprotein; transmembrane protein

Query Match
Best Local Similarity 75.0%; Score 21; DB 2; Length 1820;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FIIFGSFPTLNLFIGVITDNF 28
DB 1499 FIIFGSFPTLNLFIGVITDNF 1519

RESULT 19
S54771
sodium channel alpha subunit - human
C/Species: Homo sapiens (man)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C/Accession: S54771
R/Kruppner, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.
EMBO J. 14, 1084-1090, 1995
A/Title: Structure and functional expression of a new member of the tetrodotoxin-sensitive
A/Reference number: S54771; MUID:95237189; PMID:7720699
A/Accession: S54771
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-1977 <KLU>
A/Cross-references: UNIPROT:Q15858; EMBL:X82835; NID:9758109; PIDN:CA58042.1; PID:97581
C/Superfamily: sodium channel protein
C/Keywords: duplication

Query Match
Best Local Similarity 75.0%; Score 21; DB 2; Length 1977;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FIIFGSFPTLNLFIGVITDNF 28
DB 1429 FIIFGSFPTLNLFIGVITDNF 1449

RESULT 20
A33996
sodium channel protein I, cardiac - rat
N/Alternate names: sodium channel protein (SKM2) alpha chain
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 09-Jul-2004
C/Accession: A33996; J00412
R/Rogart, R.B.; Cribbs, L.L.; Muglia, L.K.; Kephart, D.D.; Kaiser, M.W.
Proc Natl. Acad. Sci. U.S.A. 86, 8170-8174, 1989
A/Title: Molecular cloning of a putative tetrodotoxin-resistant rat heart Na(+) channel
A/Reference number: A33996; MUID:90046760; PMID:2554302
A/Accession: A33996
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-2019 <ROG>
A/Cross-references: UNIPROT:P15389; GB:M27902; NID:9206857; PIDN:AAA42114.1; PID:9206858
R/Kallen, R.G.; Sheng, Z.H.; Yang, J.; Chen, L.; Rogart, R.B.; Barchi, R.L.
Neuron 4, 233-242, 1990
A/Title: Primary structure and expression of a sodium channel characteristic of denervat

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A/Reference number: J00412; MUID:90166613; PMID:2155010
A/Accession: J00412
A/Molecule type: mRNA
A/Residues: 1-479, 481-1712, 'T', 1714-1963, 'R', 1965-2019 <RAL>
A/Experimental source: muscle
C/Superfamily: sodium channel protein
C/Keywords: cardiac muscle; duplication; heart; sodium channel; transmembrane protein

Query Match
Best Local Similarity 75.0%; Score 21; DB 2; Length 2019;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FIIFGSFPTLNLFIGVITDNF 28
DB 1455 FIIFGSFPTLNLFIGVITDNF 1475

RESULT 21
S72458
sodium channel protein para-type alpha chain - house fly (strain Cooper)
C/Species: Musca domestica (house fly)
A/Variety: strain Cooper
C/Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C/Accession: S72458
R/Williamson, M.S.; Martinez-Torres, D.; Hick, C.A.; Devonshire, A.L.
Mol. Gen. Genet. 252, 51-60, 1996
A/Title: Identification of mutations in the housefly para-type sodium channel gene associ
A/Reference number: S72458; MUID:96397509; PMID:8804403
A/Accession: S72458
A/Molecule type: mRNA
A/Residues: 1-2108 <WIL>
A/Cross-references: UNIPROT:Q94615; EMBL:X96668
A/Experimental source: strain Cooper
C/Genetics:
A/Map position: 3
C/Superfamily: sodium channel protein
C/Keywords: alternative splicing; glycoprotein; phosphoprotein; sodium channel; transmemt
F/302,314,332,967,1451,1470/binding site: carbohydrate (asn) (covalent) #status predicted
F/541,1208,1582/binding site: phosphate (ser) (covalent) #status predicted

Query Match
Best Local Similarity 75.0%; Score 21; DB 2; Length 2108;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FIIFGSFPTLNLFIGVITDNF 28
DB 1531 FIIFGSFPTLNLFIGVITDNF 1551

RESULT 22
T43161
sodium channel protein Tuna1 - sea squirt (Halocynthia roretzi)
C/Species: Halocynthia roretzi
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43161
R/Okamura, Y.; Ono, F.; Okagaki, R.; Chong, J.; Mandel, G.
Neuron 13, 937-948, 1994
A/Title: Neutral expression of a sodium channel gene requires cell-specific interactions.
A/Reference number: Z22220; MUID:95033215; PMID:7946338
A/Accession: T43161
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-2049 <OKA>
A/Cross-references: UNIPROT:Q25150; EMBL:DJ7311; PIDN:BA04133.1
C/Superfamily: sodium channel protein
C/Keywords: sodium channel; transmembrane protein

Query Match
Best Local Similarity 64.3%; Score 18; DB 2; Length 2049;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FGSGFTLNLFIGVITDNF 28

```

DB 1522 GSPFTLNLFIGVITDNE 1539

RESULT 23

A60165 sodium channel protein - fruit fly (*Drosophila melanogaster*) (fragments)

C/Species: *Drosophila melanogaster*

C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C/Accession: S04029; A60165

R/Salkoff, L.; Butler, A.; Scavarda, N.; Wei, A.

Nucleic Acids Res. 15, 8569-8572, 1987

A/Title: Nucleotide sequence of the putative sodium channel gene from *Drosophila*: the fo

A/Reference number: S04029; MUID:88040482; PMID:2444928

A/Accession: S04029

A/Molecule type: DNA

A/Residues: 1362;363-626;627-1321 <SNL>

A/Cross-references: UNIPROT:Q27930; EMBL:X14394

R/Salkoff, L.; Butler, A.; Wei, A.; Scavarda, N.; Giffen, K.; Ifune, C.; Goodman, R.; Ma

Science 237, 744-749, 1987

A/Title: Genomic organization and deduced amino acid sequence of a putative sodium chan

A/Reference number: A60165; MUID:87292090; PMID:2441469

A/Accession: A60165

A/Status: nucleic acid sequence not shown

A/Molecule type: DNA

A/Residues: 40-355;363-560, 'P', 562-626;632-1263 <SA2>

A/Cross-references: EMBL:X14394

A/Note: part of this sequence was confirmed by mRNA sequencing

A/Note: the authors' translation is shown at position 561

A/Accession: FLYBASE:NACP60E

A/Cross-references: FLYBASE:Fgn0002920

A/Introns: 237/2; 310/3; 362/3; 414/3; 471/3; 531/3; 581/1; 626/3; 751/2; 801/1; 906/1;

Query Match 60.7%; Score 17; DB 2; Length 1321;
Best Local Similarity 100.0%; Pred. No. 2,7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GSPFTLNLFIGVITDNE 28

DB 886 GSPFTLNLFIGVITDNE 902

RESULT 24

T31092

probable voltage-gated sodium channel - *Alptasia pallida*

C/Species: *Alptasia pallida*

C/Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C/Accession: T31092

R/White, G.B.; Pfahnl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.

submitted to the EMBL Data Library, January 1998

A/Description: Structure of a putative sodium channel from the sea anemone *Alptasia pall*

A/Reference number: Z20975

A/Accession: T31092

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1810 <MHI>

A/Cross-references: UNIPROT:Q44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AA8

C/Genetics:

A/Accession: T31092

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1810 <MHI>

A/Cross-references: UNIPROT:Q44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AA8

A/Accession: T31092

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1810 <MHI>

A/Cross-references: UNIPROT:Q44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AA8

A/Accession: T31092

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1810 <MHI>

A/Cross-references: UNIPROT:Q44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AA8

C/Species: *Electrophorus electricus* (electric eel)

C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C/Accession: A03178; I50536

R/Noda, M.; Shimizu, S.; Tanabe, T.; Takai, T.; Kayano, T.; Ikeda, T.; Takahashi, H.; Na

da, H.; Miyata, T.; Numa, S.

Nature 312, 121-127, 1984

A/Title: Primary structure of *Electrophorus electricus* sodium channel deduced from cDNA

A/Reference number: A03178; MUID:85061498; PMID:6209577

A/Accession: A03178

A/Molecule type: mRNA

A/Residues: 1-1820 <MOD>

A/Cross-references: UNIPROT:P02719; GB:X01119; NID:g62776; PIDN:CAA25587.1; PID:g62777

R/Noda, M.; Numa, S.

J. Recept. Res. 7, 467-497, 1987

A/Title: Structure and function of sodium channel.

A/Reference number: I50536; MUID:87311395; PMID:2442385

A/Accession: I50536

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1820 <MOD>

A/Cross-references: GB:M2252; NID:g1041048; PIDN:AAA79960.1; PID:g1041049

C/Comment: This membrane glycoprotein mediates the voltage-dependent sodium-ion permeabil

as the membrane, the protein forms a sodium-selective channel through which sodium ions m

C/Comment: This sequence contains four highly homologous internal repeats (excluding res

Each repeat has a similar overall structure containing six subregions located in identic

has a net positive charge (S4), and one is neutral (S2).

C/Comment: The four repeating units are thought to be oriented pseudosymmetrically across

e. The presence of four homologous structures within this molecule is consistent with the

C/Comment: Available data suggest that activation and inactivation gates are located near

955 might, in conjunction with the positively charged residues of S4, act as a voltage se

C/Superfamily: sodium channel protein

C/Keywords: duplication; glycoprotein; ion transport; membrane protein; sodium channel; \

F:111-419,555-807,989-1281,1311-1587/Region: duplication internal repeats I, II, III and

F:111-411,555-585,989-1019,1311-1341/Region: S1 of repeats I through IV

F:150-171,597-620,1033-1057,1353-1376/Region: S2 of repeats I through IV

F:177-197,626-643,1062-1079,1381-1398/Region: S3 of repeats I through IV

F:204-224,651-671,1092-1112,1417-1437/Region: S4 of repeats I through IV

F:244-264,691-711,1132-1152,1454-1474/Region: S5 of repeats I through IV

F:379-402,767-790,1236-1264,1544-1567/Region: S6 of repeats I through IV

F:205,278,288,317,591,690,797,1160,1174,1806/Binding site: carbohydrate (asn) (covalent)

Query Match 53.6%; Score 15; DB 1; Length 1820;

Best Local Similarity 100.0%; Pred. No. 3.6e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 FPTLNLFIGVITDNE 28

DB 1253 FPTLNLFIGVITDNE 1267

Search completed: January 27, 2005, 17:52:46

Job time : 19 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:35:20 ; Search time 92.5 Seconds
(without alignment)
174.167 Million cell updates/sec

Title: US-10-608-584-19
Perfect score: 28
Sequence: 1 MYLYFVIFIFGSPFTLNLFIGVIIDNF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : UniProt_02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	431	2	Q62206
2	28	100.0	510	2	Q62242
3	28	100.0	742	2	Q90229
4	28	100.0	751	2	Q90228
5	28	100.0	1136	2	Q804F4
6	28	100.0	1836	1	CIN4_HUMAN
7	28	100.0	1840	1	CIN4_RAT
8	28	100.0	1840	2	Q70611
9	28	100.0	1841	2	Q9ER60
10	28	100.0	1951	1	CIN3_RAT
11	28	100.0	1951	2	Q9C007
12	28	100.0	1981	2	Q8IU06
13	28	100.0	2000	1	CIN3_HUMAN
14	28	100.0	2005	1	CIN2_HUMAN
15	28	100.0	2005	1	CIN2_RAT
16	28	100.0	2007	2	Q9YGN7
17	28	100.0	2009	1	CIN1_HUMAN
18	28	100.0	2009	1	CIN1_RAT
19	28	89.3	718	2	Q90230
20	25	89.3	743	2	Q90226
21	25	89.3	1880	2	Q9IBR1
22	25	89.3	1949	2	Q9DF53
23	25	89.3	1962	2	Q75RX9
24	25	89.3	1962	2	BAD12085
25	25	89.3	1976	2	Q63541
26	25	89.3	1976	1	CIN8_MOUSE
27	25	89.3	1978	2	CIN8_HUMAN
28	25	89.3	1980	1	CIN8_HUMAN
29	25	89.3	1984	2	Q28644
30	25	89.3	1984	2	Q08562
31	25	89.3	1988	2	Q08421

32	25	89.3	2013	2	Q865W3	Q865W3 canis fami1
33	25	89.3	2015	2	Q86UR3	Q86UR3 homo sapien
34	25	89.3	2015	2	Q81ZC9	Q81ZC9 homo sapien
35	25	89.3	2015	2	Q96J59	Q96J59 homo sapien
36	25	89.3	2016	1	CIN5_HUMAN	CIN5_HUMAN
37	25	89.3	2016	2	Q75RY0	Q75RY0 homo sapien
38	25	89.3	2016	2	BAD12084	BAD12084 homo sapi
39	25	89.3	2022	2	Q8WMP8	Q8WMP8 bos taurus
40	21	75.0	169	2	Q7PUH1	Q7PUH1 anopheles g
41	21	75.0	210	2	Q9JKCS	Q9JKCS mus musculu
42	21	75.0	296	2	Q25178	Q25178 heliothis v
43	21	75.0	576	2	Q6DLU1	Q6DLU1 aedes aegy
44	21	75.0	603	2	Q6DLT6	Q6DLT6 aedes albop
45	21	75.0	626	2	Q6DLT5	Q6DLT5 aedes albop
46	21	75.0	744	2	Q90227	Q90227 sternopygus
47	21	75.0	1130	2	Q9XZC1	Q9XZC1 boophilus m
48	21	75.0	1347	2	Q7PMT4	Q7PMT4 anopheles g
49	21	75.0	1361	2	Q7PJH0	Q7PJH0 anopheles g
50	21	75.0	1444	2	Q9UHM0	Q9UHM0 homo sapien
51	21	75.0	1689	2	Q93135	Q93135 blatella g
52	21	75.0	1695	2	Q94584	Q94584 heliothis v
53	21	75.0	1699	2	Q02037	Q02037 bdelloura c
54	21	75.0	1717	2	Q90519	Q90519 figu rubrip
55	21	75.0	1765	2	Q88457	Q88457 rattus norv
56	21	75.0	1765	2	Q9JMD4	Q9JMD4 mus musculu
57	21	75.0	1765	2	Q9R053	Q9R053 mus musculu
58	21	75.0	1784	2	Q25377	Q25377 loligo opal
59	21	75.0	1791	2	Q8NDX3	Q8NDX3 homo sapien
60	21	75.0	1791	2	Q9UHE0	Q9UHE0 homo sapien
61	21	75.0	1791	2	Q9UIH3	Q9UIH3 homo sapien
62	21	75.0	1966	2	Q925G6	Q925G6 rattus norv
63	21	75.0	1977	2	Q15858	Q15858 homo sapien
64	21	75.0	2019	1	CIN5_RAT	CIN5_RAT
65	21	75.0	2019	2	Q9JUT9	Q9JUT9 mus musculu
66	21	75.0	2031	2	Q01306	Q01306 blatella g
67	21	75.0	2031	2	Q01307	Q01307 blatella g
68	21	75.0	2051	2	Q86DI7	Q86DI7 pediculus h
69	21	75.0	2051	2	Q86DI8	Q86DI8 pediculus h
70	21	75.0	2051	2	Q86DI9	Q86DI9 pediculus h
71	21	75.0	2058	2	Q6DLT4	Q6DLT4 aedes albop
72	21	75.0	2064	2	Q6DLT3	Q6DLT3 aedes aegy
73	21	75.0	2086	2	Q86M38	Q86M38 pediculus h
74	21	75.0	2104	2	Q25440	Q25440 musca domes
75	21	75.0	2105	2	Q25439	Q25439 musca domes
76	21	75.0	2108	2	Q94615	Q94615 musca domes
77	21	75.0	2131	1	CIN4_DROME	CIN4_DROME
78	18	64.3	2049	2	Q25150	Q25150 halocynthia
79	17	60.7	281	2	Q7JN87	Q7JN87 drosophila
80	17	60.7	297	2	Q6VVE0	Q6VVE0 hirtudo medi
81	17	60.7	297	2	AAQ81289	AAQ81289 hirtudo me
82	17	60.7	1538	2	Q7PF76	Q7PF76 anopheles g
83	17	60.7	1618	2	Q8MWC7	Q8MWC7 drosophila
84	17	60.7	1810	2	Q44930	Q44930 alptasia pa
85	17	60.7	2223	2	Q7QI0V	Q7QI0V anopheles g
86	17	60.7	2304	2	Q9BMO4	Q9BMO4 blatella g
87	17	60.7	2327	2	Q9W0Y8	Q9W0Y8 drosophila
88	16	57.1	1834	2	Q28371	Q28371 equus cabal
89	15	53.6	299	2	Q6VVE1	Q6VVE1 hirtudo medi
90	15	53.6	299	2	AAQ81288	AAQ81288 hirtudo me
91	15	53.6	301	2	Q6VVE2	Q6VVE2 hirtudo medi
92	15	53.6	301	2	AAQ81287	AAQ81287 hirtudo me
93	15	53.6	1089	2	Q81S97	Q81S97 varroa deat
94	15	53.6	1820	1	CIN4_ELEBL	CIN4_ELEBL
95	15	53.6	1820	2	Q86D77	Q86D77 varroa deat
96	13	46.4	1993	2	Q90670	Q90670 apllysia cal
97	12	42.9	717	2	Q90225	Q90225 sternopygus
98	12	42.9	1695	2	Q62604	Q62604 polyorchis
99	12	42.9	1740	2	Q17314	Q17314 cyanea capi
100	12	42.9	1956	2	Q9Y5Y9	Q9Y5Y9 homo sapien

ALIGNMENTS

RESULT 1

```

ID Q62206 PRELIMINARY; PRT; 431 AA.
AC Q62206;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DR Sodium channel 3.
GN Name=Scn1a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Jover E., Shah V.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; LA2339; AAA67107.1; -.
DR HSSP; P04775; 1BYV.
DR MGD; MGI:98246; Scn1a.
DR GO; GO:0005624; C:membrane fraction; IDA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF06512; Na_trans_assoc.
DR Ion_transport; Ion_channel; Transmembrane; Transport.
SQ SEQUENCE 431 AA; 4946 MW; 9CD841FF73D1D9B7 CRC64;

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 431;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLYFVFIIFGSPFTLNLFIVGIIDNF 28
Db 357 MYLYFVFIIFGSPFTLNLFIVGIIDNF 384

RESULT 2
ID Q62242 PRELIMINARY; PRT; 510 AA.
AC Q62242;
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DE 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DR Sodium channel (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Jover E., Shah V.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; LA2341; AAA67695.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.

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DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans_1.
DR Pfam; PF00612; IQ_1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ_1.
DR PROSITE; PS50096; IQ_1.

```

```

KW Ion transport; Ion_channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
FT NON_TER 510
SQ SEQUENCE 510 AA; 58397 MW; 02DCC7DAED3796E8 CRC64;

```

```

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 510;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MYLYFVFIIFGSPFTLNLFIVGIIDNF 28
Db 1 MYLYFVFIIFGSPFTLNLFIVGIIDNF 28

RESULT 3
ID Q90229 PRELIMINARY; PRT; 742 AA.
AC Q90229;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DE 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DR Sodium channel 2 (Fragment).
OS Sternoptygia macrurus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Gymnotiformes;
OC Sternopygidae; Sternopygus.
OC NCBI_TaxID=77841;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21310016; Pubmed=11416226;
RA Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA Wilcox T.P., Zakon H.H.;
RT "Evolution and divergence of sodium channel genes in vertebrates.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7568-7592(2001).
DR EMBL; AF378140; AAK5438.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans_2.
DR Pfam; PF06512; Na_trans_assoc.
DR Ion_transport; Ion_channel; Transmembrane; Transport.
FT NON_TER 742
SQ SEQUENCE 742 AA; 84353 MW; 7F4B3003BD3F2AC4 CRC64;

```

```

Query Match
Best Local Similarity 100.0%; Score 28; DB 2; Length 742;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 MYLYFVFIIFGSPFTLNLFIVGIIDNF 28
Db 641 MYLYFVFIIFGSPFTLNLFIVGIIDNF 668

RESULT 4
ID Q90228 PRELIMINARY; PRT; 751 AA.
AC Q90228;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DE 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DR Sodium channel 3 (Fragment).

```



```

OS Sternopygus macrurus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Gymnotiformes;
OC Sternopygidae; Sternopygus.
OX NCBI_TaxID=77841;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21310016; PubMed=11416226;
RA Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA Wilcox T.P., Zakon H.H.;
RT "Evolution and divergence of sodium channel genes in vertebrates.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR EMBL; AF378141; AKS5439.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; F:cation transport; IEA.
DR GO; GO:0006812; F:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_2.
DR Pfam; PF06512; Na_trans_assoc.1.
KM Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1 1
FT NON_TER 751 751
SQ SEQUENCE 751 AA; 84598 MW; CBF6162E90A76FC CRC64;

Query Match 100.0%; Score 28; DB 2; Length 751;
Best Local Similarity 100.0%; Pred. No. 2.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIFGSPFTLNLFGVINDF 28
Db 674 MYLYFVIFIFGSPFTLNLFGVINDF 701

RESULT 5
Q804F4 PRELIMINARY; PRT; 1136 AA.
ID Q804F4;
AC Q804F4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sodium channel 7 (Fragment).
GN Name=Na7;
OS Sternopygus macrurus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Gymnotiformes;
OC Sternopygidae; Sternopygus.
OX NCBI_TaxID=77841;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu Y., Lopreato G.F., Zakon H.H.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the calcium channel alpha-1 subunits
CC family.
DR EMBL; AY183895; AAO23570.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005691; C:voltage-gated calcium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR GO; GO:0006816; F:calcium ion transport; IEA.
DR GO; GO:0006812; F:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002077; Cat_channel_TpL.
DR InterPro; IPR002111; Cat_channel_Alpha.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR010520; M_channel_nlg.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_3.
DR Pfam; PF06512; Na_trans_assoc.1.

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DR PRINTS; PR00167; CCHANNEL.
KM Calcium channel; Calcium-binding; Ion transport; Ionic channel;
KM Transmembrane; Transport; Voltage-gated channel.
FT NON_TER 1 1
FT NON_TER 1136 1136
SQ SEQUENCE 1136 AA; 129141 MW; ECD52D025B50664 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 1136;
Best Local Similarity 100.0%; Pred. No. 3.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFVIFIFGSPFTLNLFGVINDF 28
Db 1042 MYLYFVIFIFGSPFTLNLFGVINDF 1069

RESULT 6
CIN4_HUMAN STANDARD; PRT; 1836 AA.
ID CIN4_HUMAN;
AC P35499; Q15478; Q16447; Q726B1;
DT 01-JUN-1994 (Ref. 29, Created)
DT 29-MAR-2004 (Ref. 43, Last sequence update)
DT 05-JUL-2004 (Ref. 44, Last annotation update)
DE Sodium channel protein type IV alpha subunit (Voltage-gated sodium
DE channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle
DE alpha-subunit).
GN Name=SCN4A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.. AND VARIANT ASP-559.
RC TISSUE=Skeletal muscle;
RX MEDLINE=92246457; PubMed=1315496;
RA George A.L. Jr., Komisarof J., Kallen R.G., Barchi R.L.;
RT "Primary structure of the adult human skeletal muscle voltage-
RT dependent sodium channel.";
RL Ann. Neurol. 31:131-137(1992).
RN [2]
RP SEQUENCE FROM N.A..
RX MEDLINE=92134303; PubMed=1310396;
RA Wang J., Rojas C.V., Zhou J., Schwartz L.S., Nicholas H.,
RA Hoffmann E.P.;
RT "Sequence and genomic structure of the human adult skeletal muscle
RT sodium channel alpha subunit gene on 17q.";
RL Biochem. Biophys. Res. Commun. 182:794-801(1992).
RN [3]
RP SEQUENCE FROM N.A.. VARIANT MYASTHENIC SYNDROME GLU-1442, AND VARIANTS
RP LEU-246; ASP-559 AND ASN-1376.
RX MEDLINE=22684480; PubMed=12762226; DOI=10.1073/pnas.1230273100;
RA Teujino A., Maertens C., Ohno K., Shen X.-M., Fukuda T., Harper C.M.,
RA Cannon S.C., Engel A.G.;
RT "Myasthenic syndrome caused by mutation of the SCN4A sodium channel.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7377-7382(2003).
RN [4]
RP SEQUENCE FROM N.A.. AND VARIANT ASN-1376.
RX MEDLINE=9338444; PubMed=1339144;
RA McLatchey A.I., Lin C.S., Wang J., Hoffmann E.P., Rojas C.V.,
RA Guisella J.F.;
RT "The genomic structure of the human skeletal muscle sodium channel
RT gene.";
RL Hum. Mol. Genet. 1:521-521(1992).
RN [5]
RP SEQUENCE OF 1305-1339 FROM N.A.. AND VARIANTS PMC VAL-1306 AND
RP MET-1313.
RX MEDLINE=92154689; PubMed=1310898;
RA McLatchey A.I., van den Bergh P., Pericak-Vance M.A., Raskind W.,
RA Verellen G., McKenna-Yasek D., Rao K., Haines J.L., Bird T.,
RA Brown R.H. Jr., Guisella J.F.;
RT "Temperature-sensitive mutations in the III-IV cytoplasmic loop region
RT of the skeletal muscle sodium channel gene in paramyotonia
RT congenita.";

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RL Cell 68:769-774(1992).
 RN [6]
 RP VARIANT HYP MET-704.
 RX MEDLINE=92069747; PubMed=1659948;
 RA Pracek L.J., George A.L. Jr., Griggs R.C., Tawil R., Kallen R.G.,
 RT Barclai R.L., Robertson M., Leppert M.F.;
 RT "Identification of a mutation in the gene causing hyperkalemic
 RT periodic paralysis.";
 RL Cell 67:1021-1027(1991).
 RN [7]
 RP VARIANT HYP VAL-1592.
 RX MEDLINE=92065978; PubMed=1659668;
 RA Rojas C.V., Wang J., Schwartz U.S., Hoffman E.P., Powell B.R.,
 RT Brown R.H. Jr.;
 RT "A Met-to-Val mutation in the skeletal muscle Na⁺ channel alpha-
 RT subunit in hyperkalemic periodic paralysis.";
 RL Nature 354:387-389(1991).
 RN [8]
 RP VARIANTS PMC PHE-804 AND THR-1156.
 RX MEDLINE=93265141; PubMed=1338909;
 RA McIlatchey A.I., McKenna-Yasek D., Cros D., Worthen H.G., Kuncel R.W.,
 RT Desliya S.M., Cornblath D.R., Gusella J.F., Brown R.H. Jr.;
 RT "Novel mutations in families with unusual and variable disorders of
 RT the skeletal muscle sodium channel.";
 RL Nat. Genet. 2:148-152(1992).
 RN [9]
 RP VARIANTS PMC CYS-1448 AND HIS-1448.
 RX MEDLINE=92265302; PubMed=1316765;
 RA Pracek L.J., George A.L. Jr., Barclai R.L., Griggs R.C., Riggs J.E.,
 RT Robertson M., Leppert M.F.;
 RT "Mutations in an S4 segment of the adult skeletal muscle sodium
 RT channel cause paramyotonia congenita.";
 RL Neuron 8:891-897(1992).
 RN [10]
 RP VARIANT PMC ARG-1433.
 RX MEDLINE=93270429; PubMed=8388676;
 RA Pracek L.J., Gowu L., Kwietcinski H., McManis P., Wendell J.R.,
 RT Barclai R.L., George A.L. Jr., Barclai R.L., Robertson M., Leppert M.F.;
 RT "Sodium channel mutations in paramyotonia congenita and hyperkalemic
 RT periodic paralysis.";
 RL Ann. Neurol. 33:300-307(1993).
 RN [11]
 RP VARIANTS PMC ALA-1306, GLU-1306 AND VAL-1306.
 RX MEDLINE=94141728; PubMed=8308722;
 RA Lerche H., Heine R., Pika U., George A.L. Jr., Mitrovic N.,
 RT Browatzki M., Weiss T., Rivet-Bastide M., Franke C., Lomonaco M.,
 RT Ricker K., Lehmann-Horn F.;
 RT "Human sodium channel myotonia: slowed channel inactivation due to
 RT substitutions for a glycine within the III-IV linker.";
 RL J. Physiol. (Lond.) 470:113-22(1993).
 RN [12]
 RP VARIANT PMC MET-1589.
 RX MEDLINE=94061027; PubMed=8242056;
 RA Heine R., Pika U., Lehmann-Horn F.;
 RT "A novel SCN4A mutation causing myotonia aggravated by cold and
 RT potassium.";
 RL Hum. Mol. Genet. 2:1349-1353(1993).
 RN [13]
 RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA VAL-1160.
 RX PubMed=8058156;
 RA Ptacek L.J., Tawil R., Griggs R.C., Meola G., McManis P., Barclai R.L.,
 RT Mendell J.R., Harris C., Spitzer R., Santiago F., Leppert M.F.;
 RT "Sodium channel mutations in acetazolamide-responsive myotonia
 RT congenita, paramyotonia congenita, and hyperkalemic periodic
 RT paralysis.";
 RL Neurology 44:1500-1503(1994).
 RN [14]
 RP VARIANT PARAMYOTONIA WITHOUT COLD PARALYSIS ILE-1293.
 RX MEDLINE=96154961; PubMed=8580427;
 RA Koch M.C., Baumach K., George A.L., Ricker K.,
 RT "Paramyotonia congenita without paralysis on exposure to cold: a novel
 RT mutation in the SCN4A gene (Val1293Ile).";
 RL NeuroReport 6:2001-2004(1995).

RN [15]
 RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA MET-445.
 RX PubMed=9392583;
 RA Rosenfeld J., Sloan-Brown K., George A.L. Jr.;
 RT "A novel muscle sodium channel mutation causes painful congenital
 RT myotonia.";
 RL Ann. Neurol. 42:811-814(1997).
 RN [16]
 RP VARIANT POTASSIUM-AGGRAVATED MYOTONIA MET-445.
 RX PubMed=10218481;
 RA Wang D.W., Vandecastee D., Ruben P.C., George A.L. Jr., Bennett P.B.,
 RT "Functional consequences of a domain 1/S6 segment sodium channel
 RT mutation associated with painful congenital myotonia.";
 RL FEBS Lett. 448:231-234(1999).
 RN [17]
 RP VARIANT HYPOKPP HIS-669.
 RX PubMed=10599760;
 RA Bulman D.E., Scoggan K.A., van Oene M.D., Nicolle M.W., Hahn A.F.,
 RT Tollar L.L., Ebers G.C.;
 RT "A novel sodium channel mutation in a family with hypokalemic periodic
 RT paralysis.";
 RL Neurology 53:1932-1936(1999).
 RN [18]
 RP VARIANT HYPOKPP SER-1158.
 RX PubMed=10851391;
 RA Sugita Y., Aoki T., Sugiyama Y., Hida C., Ogata M., Yamamoto T.;
 RT "Temperature-sensitive sodium channelopathy with heat-induced myotonia
 RT and cold-induced paralysis.";
 RL Neurology 54:2179-2181(2000).
 RN [19]
 RP VARIANTS HYPOKPP GLY-672 AND HIS-672.
 RX PubMed=10944223;
 RA Jurkat-Rott K., Mitrovic N., Hang C., Kouzmekine A., Ialzo P.,
 RT Herzog J., Lerche H., Nicole S., Vale-Santos J., Chauveau D.,
 RT Fontaine B., Lehmann-Horn F.;
 RT "Voltage-sensor sodium channel mutations cause hypokalemic periodic
 RT paralysis type 2 by enhanced inactivation and reduced current.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9549-9554(2000).
 RN [20]
 RP VARIANT HYPOKPP SER-672.
 RX PubMed=11558801;
 RA Bendahhou S., Cummins T.R., Griggs R.C., Fu Y.H., Ptacek L.J.;
 RT "Sodium channel inactivation defects are associated with
 RT acetazolamide-exacerbated hypokalemic periodic paralysis.";
 RL Ann. Neurol. 50:417-420(2001).
 RN [21]
 RP VARIANT HYPOKPP SER-672.
 RX PubMed=11591859;
 RA Davies N.P., Bunson L.H., Samuel M., Hanna M.G.;
 RT "Sodium channel gene mutations in hypokalemic periodic paralysis: an
 RT uncommon cause in the UK.";
 RL Neurology 57:1323-1325(2001).
 CC -1- FUNCTION: This protein mediates the voltage-dependent sodium ion
 CC permeability of excitable membranes. Assuming opened or closed
 CC conformations in response to the voltage difference across the
 CC membrane, the protein forms a sodium-selective channel through
 CC which Na⁺ ions may pass in accordance with their electrochemical
 CC gradient. This sodium channel may be present in both denervated
 CC and innervated skeletal muscle.
 CC -1- SUBUNIT: Muscle sodium channels contain an alpha subunit and a
 CC smaller beta subunit. Interacts with the PDZ domain of the
 CC synaptrophin SNTRL, SNRBI and SNRIB (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- DISEASE: Defects in SCN4A are the cause of paramyotonia congenita
 CC of von Bultenborg (PMC) [MIM:168300]. PMC is an autosomal dominant
 CC sodium channel disease characterized by myotonia, increased by
 CC exposure to cold, intermittent flaccid paresis, not necessarily

Query Match 100.0%; Score 28; DB 1; Length 1836;
 Best Local Similarity 100.0%; Pred. No. 5, 1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLYFVFIIFGSEFTNLFGVIIDNF 28
 DB 1271 MYLYFVFIIFGSEFTNLFGVIIDNF 1298

RESULT 7
 ID CINA_RAT STANDARD; PRT; 1840 AA.
 AC P15350;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel protein type IV alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.4) (Sodium channel protein, skeletal muscle alpha-subunit) (Mu-1).
 GN Name=Scn4a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP MEDLINE=90148778; PubMed=2559760;
 RA Trimmer J.S., Cooperman S.S., Tomiko S.A., Zhou J., Crean S.M., Boyle M.B., Kallen R.G., Sheng Z., Barchi R.L., Sigworth F.J., Goodman R.H., Agnew W.S., Mandel G.;
 RT "Primary structure and functional expression of a mammalian skeletal muscle sodium channel.";
 RT Neuron 33:33-49(1989).
 RL

CC -1- FUNCTION: This protein mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na⁺ ions may pass in accordance with their electrochemical gradient. This sodium channel may be present in both denervated and innervated skeletal muscle.
 CC -1- SUBUNIT: Muscle sodium channels contain an alpha subunit and a smaller beta subunit. Interacts with the PDZ domain of the synaptobrevin SNTA1, SNTB1 and SNTB2 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements> or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: M26643; AAA41682.1; -.
 CC PIR: J00007; CHRTM1.
 CC HSSP: P04775; 1BYT.
 CC InterPro: IPR001682; Ca/Na_pore.
 CC InterPro: IPR002111; Cat_channel_TrpL.
 CC InterPro: IPR005821; Ion trans.
 CC InterPro: IPR000048; IQ region.
 CC InterPro: IPR005820; Na_channel_nlg.
 CC InterPro: IPR001696; Na_channel.
 CC InterPro: IPR008052; Na_channel4.
 CC InterPro: IPR010526; Na_trans_assoc.
 CC Pfam: PF00520; Ion trans; 4.
 CC Pfam: PF00612; IQ_1.

DR Pfam; PF06512; Na trans assoc; 1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR PRINTS; PRO1665; NACHANNEL4.
 DR PROSITE; PS50096; IQ_1.
 KW Glycophorin; Ion transport; Ionic channel; Multigene family;
 KW Phosphorylation; Repeat; Sodium channel; Transmembrane;
 KW Voltage-gated channel.
 FT TRANSMEM 130 152 S1 of repeat I.
 FT TRANSMEM 156 179 S2 of repeat I.
 FT TRANSMEM 192 212 S3 of repeat I.
 FT TRANSMEM 214 233 S4 of repeat I.
 FT TRANSMEM 252 274 S5 of repeat I.
 FT TRANSMEM 417 444 S6 of repeat I.
 FT TRANSMEM 571 593 S1 of repeat II.
 FT TRANSMEM 663 685 S2 of repeat II.
 FT TRANSMEM 696 721 S3 of repeat II.
 FT TRANSMEM 722 737 S4 of repeat II.
 FT TRANSMEM 756 778 S5 of repeat II.
 FT TRANSMEM 832 859 S6 of repeat II.
 FT TRANSMEM 1084 1105 S1 of repeat III.
 FT TRANSMEM 1117 1140 S2 of repeat III.
 FT TRANSMEM 1149 1168 S3 of repeat III.
 FT TRANSMEM 1176 1195 S4 of repeat III.
 FT TRANSMEM 1215 1236 S5 of repeat III.
 FT TRANSMEM 1324 1351 S6 of repeat III.
 FT TRANSMEM 1405 1427 S1 of repeat IV.
 FT TRANSMEM 1437 1460 S2 of repeat IV.
 FT TRANSMEM 1468 1487 S3 of repeat IV.
 FT TRANSMEM 1502 1522 S4 of repeat IV.
 FT TRANSMEM 1535 1556 S5 of repeat IV.
 FT TRANSMEM 1627 1653 S6 of repeat IV.
 FT DOMAIN 1720 1749 IQ.
 FT CARBOHYD 288 288 N-linked (GlcNAc...)
 FT CARBOHYD 291 291 N-linked (GlcNAc...)
 FT CARBOHYD 297 297 N-linked (GlcNAc...)
 FT CARBOHYD 303 303 N-linked (GlcNAc...)
 FT CARBOHYD 309 309 N-linked (GlcNAc...)
 FT CARBOHYD 315 315 N-linked (GlcNAc...)
 FT CARBOHYD 327 327 N-linked (GlcNAc...)
 FT CARBOHYD 356 356 N-linked (GlcNAc...)
 FT CARBOHYD 502 502 N-linked (GlcNAc...)
 FT CARBOHYD 954 954 N-linked (GlcNAc...)
 FT CARBOHYD 1198 1198 N-linked (GlcNAc...)
 FT MOD_RES 56 56 Phosphoserine (by PKA)
 FT MOD_RES 251 251 Phosphoserine (by PKA)
 FT MOD_RES 1321 1321 Phosphoserine (by PKA)
 FT MOD_RES 1504 1504 Phosphoserine (by PKA)
 SQ SEQUENCE 1840 AA; 20865 MW; C5DC09D93DD9FAD6 CRC64;

Query Match 100.0%; Score 28; DB 1; Length 1840;
 Best Local Similarity 100.0%; Pred. No. 5, 1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLYFVFIIFGSEFTNLFGVIIDNF 28
 DB 1264 MYLYFVFIIFGSEFTNLFGVIIDNF 1291

RESULT 8
 ID 070611 PRELIMINARY; PRT; 1840 AA.
 AC 070611;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Rat skeletal muscle type 1 voltage-gated sodium channel (RSKM1) variant.
 GN Name=SCN4a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=Copenhagen; TISSUE=Prostate;
RA MEDLINE=98273645; PubMed=9613589;
RA Dias J.K.J., Stewart D., Fraser S.P., Black J.A., Dibb-Hajj S.,
RA Maxam S.G., Archer S.N., Djamgoz M.B.A.,
RT "Expression of skeletal muscle-type voltage-gated Na+ channel in rat
RL FEBS Lett. 427:5-10(1998).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL, Y17153; CAA7659.1; -.
DR HSSP, P04775; IBBY.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR GO: GO:0005261; C:voltage-gated sodium channel complex; IEA.
DR GO: GO:0005261; F:cation channel activity; IEA.
DR GO: GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO: GO:0006814; P:cation transport; IEA.
DR GO: GO:0006814; P:sodium ion transport; IEA.
DR InterPro: IPR001682; Ca/Na pore.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR005821; Ion_trans.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR005820; M_channel_nlg.
DR InterPro: IPR001696; Na_channel.
DR InterPro: IPR008052; Na_channel.
DR Pfam: PF00520; Ion_trans_4.
DR Pfam: PF00612; IQ_1.
DR Pfam: PF06512; Na_trans_assoc_1.
DR PRINTS: PR00170; NACHANNEL.
DR PRINTS: PR01665; NACHANNEL4.
DR SMART: SM00015; IQ_1.
DR PROSITE: PS50096; IQ_1.
KM Ion transport; Ionic channel; Sodium channel; Transmembrane;
KM Transport; Voltage-gated channel.
SQ SEQUENCE 1840 AA; 208823 MW; BIDFPA538E264B40 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 1840;
Best Local Similarity 100.0%; Pred. No. 5,1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLYFVIFIIIFGSPFTLNIFGIYIDNF 28
Db 1264 MYLYFVIFIIIFGSPFTLNIFGIYIDNF 1291

RESULT 9
Q9ER60 PRELIMINARY; PRT; 1841 AA.
AC Q9ER60;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Voltage-gated sodium channel.
GN Name=Scn4a;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=balb/c; TISSUE=Heart;
RA MEDLINE=21823196; PubMed=11834499;
RA Zimmer T., Bendorf K.;
RT "The mouse heart sodium channel (mH1): cloning and characterization of
RT alternatively spliced variants."
RL Am. J. Physiol. Heart Circ. Physiol. 282:H1007-H1017(2002).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC EMBL: AJ778787; CAC1746.1; -.
DR HSSP: P04775; IBBY.
DR MGD: MGI:98250; Scn4a.
GO: GO:0016021; C:Integral to membrane; IEA.

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DR GO: GO:0005158; C:voltage-gated sodium channel complex; IEA.
DR GO: GO:0005261; F:cation channel activity; IEA.
DR GO: GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO: GO:0006814; P:cation transport; IEA.
DR InterPro: IPR001682; Ca/Na pore.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR005821; Ion_trans.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR005820; M_channel_nlg.
DR InterPro: IPR001696; Na_channel.
DR InterPro: IPR008052; Na_channel.
DR InterPro: IPR010526; Na_trans_assoc.
DR Pfam: PF00520; Ion_trans_4.
DR Pfam: PF00612; IQ_1.
DR Pfam: PF06512; Na_trans_assoc_1.
DR PRINTS: PR00170; NACHANNEL.
DR PRINTS: PR01665; NACHANNEL4.
DR SMART: SM00015; IQ_1.
DR PROSITE: PS50096; IQ_1.
KM Ion transport; Ionic channel; Sodium channel; Transmembrane;
KM Transport; Voltage-gated channel.
SQ SEQUENCE 1841 AA; 208796 MW; 0766PDD3A9E0B55 CRC64;

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Query Match 100.0%; Score 28; DB 2; Length 1841;
Best Local Similarity 100.0%; Pred. No. 5,1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLYFVIFIIIFGSPFTLNIFGIYIDNF 28
Db 1265 MYLYFVIFIIIFGSPFTLNIFGIYIDNF 1292

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RESULT 10
CIN3_RAT STANDARD; PRT; 1951 AA.
ID CIN3_RAT
AC P08104;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sodium channel protein type III alpha subunit (Voltage-gated sodium
DE channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha
DE subunit) (Voltage-gated sodium channel subtype III).
GN Name=Scn3a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RA MEDLINE=88137594; PubMed=249363;
RA Kayano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
RT "Primary structure of rat brain sodium channel III deduced from the
RT cDNA sequence."
RL FEBS Lett. 228:187-194(1988).
CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC of excitable membranes. Assuming opened or closed conformations in
CC response to the voltage difference across the membrane, the
CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC 3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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$$R_N[1] =$$
$$R_N[1] =$$

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RP SEQUENCE FROM N.A.
RC TISSUE=Normal brain;
RA Ouchida M., Ohmori I.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AB098335; BAC45228.1; -.
DR HSPB1; P04775; IBY.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:000612; P:cation transport; IEA.
DR GO; GO:000614; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IO_region.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR008051; Na_channel1.
DR InterPro; IPR010526; Na_trans_assoc.
DR InterPro; IPR000100; Ribonuclease_P.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF06512; IO_1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PRINTS; PR01664; NACHANNEL.
DR SMART; SM00015; IO_1.
DR PROSITE; PS00648; RIBONUCLEASE_P; UNKNOWN 1.
KM Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1981 AA; 226201 MW; B1D6946D6491B7AD CRC64;

Query Match      100.0%; Score 28; DB 2; Length 1981;
Best Local Similarity 100.0%; Pctd. No. 5.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYLFFVFIIFGSEFTLNFIVGIINNF 28
DQ 1431 MYLFFVFIIFGSEFTLNFIVGIINNF 1458

RESULT 13
CIN3_HUMAN
ID CIN3_HUMAN STANDARD; PRT; 2000 AA.
AC Q9NY46; Q16142; Q9BZB3; Q9C066; Q9NYK2; Q9UPD1; Q9Y6P4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sodium channel protein type III alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha subunit) (Voltage-gated sodium channel subtype III).
GN Name=SCN3A; Synonyms=NA3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA Chen Y., Dale T.J., Romanos M.A., Whitaker W.R., Xie X., Clare J.J.;
RT "Cloning, distribution and functional analysis of the human brain type III sodium channel from human brain."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Jeong S.-Y., Goto J., Kanazawa I.;
RT "Cloning of cDNA for human voltage-gated sodium channel alpha subunit, SCN3A."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), AND VARIANT THR-606.

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RX MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA Kasai N., Fukushina K., Ueki Y., Praad S., Nosakowski J.,
RA Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT "Genomic structures of SCN2A and SCN3A - candidate genes for deafness at the DFNB16 locus."
RL Gene 264:113-122(2001).
RN [4]
RP SEQUENCE OF 1-1415 FROM N.A. (ISOFORMS 2 AND 4).
RC TISSUE=Brain;
RX MEDLINE=98251277; PubMed=9589372;
RA Lu C.M., Brown G.B.;
RT "Isolation of a human-brain sodium-channel gene encoding two isoforms of the subtype III alpha-subunit."
RL J. Mol. Neurosci. 10:67-70(1998).
RN [5]
RP SEQUENCE OF 1324-1413 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94211784; PubMed=8159690;
RA Malo M.S., Stivastava K., Andresen J.M., Chen X.N., Korenberg J.R.,
RA Ingram V.M.;
RT "Targeted gene walking by low stringency polymerase chain reaction: assignment of a putative human brain sodium channel gene (SCN3A) to chromosome 2q24-31."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2975-2979(1994).
RN [6]
RP SEQUENCE OF 1669-1750 FROM N.A.
RC TISSUE=Kidney;
RA Tonkovich G.S., Kyle J.W.;
RT "Endogenous sodium current in HEK293 cells: increase in cell surface expression of endogenous currents by stable transfection of the Beta 1 subunit."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Exons 6A and 6N only differ by a single residue;
CC Name=1; Synonyms=6A-12-12b;
CC IsoId=Q9NY46-1; Sequence=Displayed;
CC Name=2; Synonyms=6A-12;
CC IsoId=Q9NY46-2; Sequence=VSP_001034;
CC Name=3; Synonyms=6N-12-12b;
CC IsoId=Q9NY46-3; Sequence=VSP_001033;
CC Name=4; Synonyms=6N-12;
CC IsoId=Q9NY46-4; Sequence=VSP_001033;
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IO domain.
CC -----
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CC -----
DR EMBL; AJ251507; CAB85895.1; -.
DR EMBL; AF225987; AK00219.1; -.
DR EMBL; AF330135; AAG53414.1; -.
DR EMBL; AF330118; AAG53414.1; JOINED.
DR EMBL; AF330119; AAG53414.1; JOINED.
DR EMBL; AF330120; AAG53414.1; JOINED.

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DR	EMBL; AF330121;	AAG53414.1;	JOINED.
DR	EMBL; AF330122;	AAG53414.1;	JOINED.
DR	EMBL; AF330123;	AAG53414.1;	JOINED.
DR	EMBL; AF330124;	AAG53414.1;	JOINED.
DR	EMBL; AF330125;	AAG53414.1;	JOINED.
DR	EMBL; AF330126;	AAG53414.1;	JOINED.
DR	EMBL; AF330127;	AAG53414.1;	JOINED.
DR	EMBL; AF330128;	AAG53414.1;	JOINED.
DR	EMBL; AF330129;	AAG53414.1;	JOINED.
DR	EMBL; AF330130;	AAG53414.1;	JOINED.
DR	EMBL; AF330131;	AAG53414.1;	JOINED.
DR	EMBL; AF330132;	AAG53414.1;	JOINED.
DR	EMBL; AF330133;	AAG53414.1;	JOINED.
DR	EMBL; AF330134;	AAG53415.1;	JOINED.
DR	EMBL; AF330135;	AAG53415.1;	JOINED.
DR	EMBL; AF330136;	AAC29514.1;	-.
DR	EMBL; AF330137;	AAB30530.1;	-.
DR	EMBL; AF330138;	AAR4690.1;	-.
DR	HSP; A54937;	A54937.	
DR	HSP; P04775;	IBYI.	
DR	Genew; HGNC:10590;	SCN3A.	
DR	MIM; 182391;	-.	
DR	GO; GO:0001518;	C:voltage-gated sodium channel complex; NAS.	
DR	GO; GO:0005548;	F:sodium-gated sodium channel activity; NAS.	
DR	GO; GO:0006814;	P:sodium ion transport; NAS.	
DR	InterPro; IPR001682;	Ca/Na pore.	
DR	InterPro; IPR002111;	Cat channel_TPL.	
DR	InterPro; IPR005821;	Ion trans.	
DR	InterPro; IPR005820;	IQ region.	
DR	InterPro; IPR001686;	M+channel nlg.	
DR	InterPro; IPR010526;	Na_channel.	
DR	Pfam; PF00520;	Ion_trans_4.	
DR	Pfam; PF06612;	IQ_1.	
DR	Pfam; PF06512;	Na_trans_assoc; 1.	
DR	PRINTS; PR00170;	NACHANNEL.	
DR	PROSITE; PSS0096;	IQ_1.	
KM	Alternative splicing; Glycoprotein; Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat; Sodium channel; Transmembrane, Voltage-gated channel.		
FT	TRANSMEM	124	147
FT	TRANSMEM	156	175
FT	TRANSMEM	189	207
FT	TRANSMEM	214	233
FT	TRANSMEM	249	273
FT	TRANSMEM	401	426
FT	TRANSMEM	755	779
FT	TRANSMEM	791	814
FT	TRANSMEM	823	842
FT	TRANSMEM	849	869
FT	TRANSMEM	885	905
FT	TRANSMEM	959	984
FT	TRANSMEM	1202	1225
FT	TRANSMEM	1239	1264
FT	TRANSMEM	1271	1292

Query Match	Best Local Similarity	100.0%	Score 28;	DB 1;	Length 2000;
Matches 28;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
1 MYLFPVFIIFGSPFLNLFICVITIDNF 28	1444 MYLFPVFIIFGSPFLNLFICVITIDNF 1471				
RESULT 14					
CIN2_HUMAN	STANDARD;	PRT;	2005	AA.	
AC Q99250; Q14472; Q9B2C9; Q9B2D0;					
DT 01-JUN-1994 (Rel. 29, Created)					
DT 28-FEB-2003 (Rel. 41, Last sequence update)					
DT 05-JUL-2004 (Rel. 44, Last annotation update)					
DE Sodium channel protein type II alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha subunit) (HBSIC II).					
DB Name=SCN2A; Synonyms=SCN2A2, NAC2;					
OS Homo sapiens (human).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OC NCBI_TaxID=9606;					
[1]					
SEQUENCE FROM N.A. (ISOFORM 1).					
RC TISSUE=Brain;					
RX MEDLINE=92390418, PubMed=1325650;					
RA Ahmed C.M., Ware D.H., Lee S.C., Patten C.D., Ferrer-Montiel A.V.,					
RA Schindler A.F., McPherson J.D., Wagner-McPherson C.B., Wasmuth J.J.,					
RA Evans G.A., Montiel M.;					
RT "Primary structure, chromosomal localization, and functional					
RT expression of a voltage-gated sodium channel from human brain.",					
RL Proc. Natl. Acad. Sci. U.S.A. 89:8220-8224 (1992).					
[2]					
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).					
RP MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;					
RA Keelani N., Pukushim K., Ueki Y., Prasad S., Nozakowski J.,					
RA Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.,					
RT "Genomic structures of SCN2A and SCN3A - candidate genes for deafness					
RT at the DNRA16 locus.",					
RL Gene 264:113-122 (2001).					
[3]					
SEQUENCE OF 1-89 FROM N.A.					
RP Lu C.-M., Eichelberger J.S., Beckman M.L., Schade S.D., Brown G.B.,					
RT "Isolation of the 5'-flanking region for human brain sodium channel					


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RT subtype II alpha-Subunit (SCN2A).";
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1702-2005 FROM N.A.
RC TISSUE=Brain.
RX MEDLINE=92275082; PubMed=1317301;
RA Lu C.-M., Han U., Rado T.A., Brown G.B.;
RT "Differential expression of two sodium channel subtypes in human
RL brain."
RT FEBS Lett. 303:53-58(1992).
RN [5]
RP SEQUENCE OF 1702-1772 FROM N.A.
RX MEDLINE=9110524; PubMed=184640;
RA Han U., Lu C.-M., Brown G.B., Rado T.A.;
RT "Direct amplification of a single dissected chromosomal segment by
RT polymerase chain reaction: a human brain sodium channel gene is on
RT chromosome 2q22-q23."
RT Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
CC of excitable membranes. Assuming opened or closed conformations in
CC response to the voltage difference across the membrane, the
CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC 3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Adult, 6A;
CC IsoId=Q99250-1; Sequence=Displayed;
CC Name=2; Synonyms=Neonatal, 6N;
CC IsoId=Q99250-2; Sequence=VSP_001032;
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M94055; AAA18895.1; -
DR EMBL; AF059683; AAC14574.1; -
DR EMBL; AF327246; AAG53413.1; JOINED.
DR EMBL; AF327226; AAG53413.1; JOINED.
DR EMBL; AF327227; AAG53413.1; JOINED.
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DR EMBL; AF327229; AAG53413.1; JOINED.
DR EMBL; AF327230; AAG53413.1; JOINED.
DR EMBL; AF327231; AAG53413.1; JOINED.
DR EMBL; AF327232; AAG53413.1; JOINED.
DR EMBL; AF327233; AAG53413.1; JOINED.
DR EMBL; AF327234; AAG53413.1; JOINED.
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DR EMBL; M91804; -; NOT ANNOTATED_CDS.
DR EMBL; M55662; AAB65854.2; -
DR HSSP; P04775; 1BYX.
DR Gene: HGNC:10588; SCN2A2.
DR MIM; 601219; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; TAS.
DR GO; GO:0006814; P:sodium ion transport; TAS.
DR InterPro; IPR001682; Ca/Na.pore.
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DR InterPro; IPR000821; Ion_channel.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF00612; IQ_1.
DR Pfam; PF05512; Na_trans_assoc_1.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PSS0096; IQ_1.
DR KX Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
DR KW Multigene family; Repeat; Sodium channel; Transmembrane;
KW Voltage-gated channel.
FT REPEAT 111 456
FT REPEAT 741 1013
FT REPEAT 1190 1504
FT REPEAT 1513 1811
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FT TRANSMEM 157 176
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FT TRANSMEM 790 813
FT TRANSMEM 822 841
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FT TRANSMEM 1663 1685
FT TRANSMEM 1752 1776
FT DOMAIN 1905 1934
FT CARBOHYD 212 212

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N-linked (GlcNAc. . .) (Potential).


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FT CARBOHYD 285 285 N-linked (GlcNAc... ) (Potential)
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FT CARBOHYD 297 297 N-linked (GlcNAc... ) (Potential)
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FT CARBOHYD 308 308 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 340 340 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 604 604 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 624 624 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 883 883 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1055 1055 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1072 1072 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1136 1136 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1368 1368 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1382 1382 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1393 1393 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1778 1778 N-linked (GlcNAc... ) (Potential)
FT VARSPLIC 209 209 D -> N (in isoform 2).
FT CONFLICT 524 524 /FTId=VSP_001032.
Query Match 100.0%; Score 28; DB 1; Length 2005;
Beet Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MLYLVFIPIFGSFTLNLFIVGIIDNF 28
Db 1449 MLYLVFIPIFGSFTLNLFIVGIIDNF 1476
RESULT 15
ID CIN2_RAT STANDARD; PRT; 2005 AA.
AC P04775;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sodium channel protein type II alpha subunit (Voltage-gated sodium
channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
subunit).
GN Name=Scn2a;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86146901; PubMed=3754035;
RA Node M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kurasaki M.,
RA Takehashi H., Numa S.;
RT "Existence of distinct sodium channel messenger RNAs in rat brain.";
RL Nature 320:186-192(1986).
CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
of excitable membranes. Assuming opened or closed conformations in
response to the voltage difference across the membrane, the
protein forms a sodium-selective channel through which Na(+) ions
may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
segment (S4). Segments S4 are probably the voltage-sensors and are
characterized by a series of positively charged amino acids at
every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
-----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL, X03639; CA27287.1; -.
DR PDB; 1BY7; NMR; A=1474-1526.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrypL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; Ion_region.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF06512; IQ; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS50096; IQ; 1.
KW 3D-structure; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Repeat; Sodium channel; Transmembrane;
KW Voltage-gated channel.
FT REPEAT 111 456 I.
FT REPEAT 741 1013 II.
FT REPEAT 1190 1504 III.
FT REPEAT 1513 1811 IV.
FT TRANSMEM 125 148 S1 of repeat I.
FT TRANSMEM 157 176 S2 of repeat I.
FT TRANSMEM 190 208 S3 of repeat I.
FT TRANSMEM 215 234 S4 of repeat I.
FT TRANSMEM 251 274 S5 of repeat I.
FT TRANSMEM 402 427 S6 of repeat I.
FT TRANSMEM 754 778 S1 of repeat II.
FT TRANSMEM 813 833 S2 of repeat II.
FT TRANSMEM 822 841 S3 of repeat II.
FT TRANSMEM 848 867 S4 of repeat II.
FT TRANSMEM 884 904 S5 of repeat II.
FT TRANSMEM 958 983 S6 of repeat II.
FT TRANSMEM 1204 1227 S1 of repeat III.
FT TRANSMEM 1241 1266 S2 of repeat III.
FT TRANSMEM 1273 1294 S3 of repeat III.
FT TRANSMEM 1299 1320 S4 of repeat III.
FT TRANSMEM 1340 1367 S5 of repeat III.
FT TRANSMEM 1447 1473 S6 of repeat III.
FT TRANSMEM 1527 1550 S1 of repeat IV.
FT TRANSMEM 1562 1585 S2 of repeat IV.
FT TRANSMEM 1592 1615 S3 of repeat IV.
FT TRANSMEM 1626 1647 S4 of repeat IV.
FT TRANSMEM 1663 1685 S5 of repeat IV.
FT TRANSMEM 1752 1776 S6 of repeat IV.
FT DOMAIN 1905 1934 IQ.
FT CARBOHYD 212 212 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 285 285 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 291 291 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 297 297 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 303 303 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 308 308 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 340 340 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 360 360 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 604 604 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 624 624 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 883 883 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1055 1055 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1072 1072 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1136 1136 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1368 1368 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1382 1382 N-linked (GlcNAc... ) (Potential)
FT CARBOHYD 1393 1393 N-linked (GlcNAc... ) (Potential)
SQ SEQUENCE 2005 AA; 227872 MW; 861BE583D79F8324 CRC64;
Query Match 100.0%; Score 28; DB 1; Length 2005;
Beet Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MLYLVFIPIFGSFTLNLFIVGIIDNF 28
Db 1449 MLYLVFIPIFGSFTLNLFIVGIIDNF 1476
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RESULT 16
09YGN7 PRELIMINARY; PRT; 2007 AA.
ID 09YGN7
AC 09YGN7;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Voltage-dependent sodium channel.
OS Cynops pyrrhogaster (Japanese common newt).
OC Amphibia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RA Hirota K., Kaneko Y., Matsumoto G., Hanyu Y.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC EMBL; AF123593; AAD17315.1; -.
DR HSBP; P04775; IBY.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0003158; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF06512; IQ_1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 2007 AA; 228398 MW; 013B9B9EC9C294C9 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 2007;
Best Local Similarity 100.0%; Pred. No. 5.5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLYPFIIFIPSGFTLNFIQVITDNF 28
Db 1450 MWLYPFIIFIPSGFTLNFIQVITDNF 1477

RESULT 17
CINI1 HUMAN STANDARD; PRT; 2009 AA.
ID CINI1 HUMAN
AC P35458; Q16172; Q96LA3; Q9CC08;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Sodium channel protein type I alpha subunit (Voltage-gated sodium
DE channel alpha subunit Nav1.1) (Sodium channel protein, Brain I alpha
DE subunit)
GN Name=SCN1A; Synonyms=SCN1, NAC1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GFS+2 MET-875 AND
RP HIS-1648.
RX MEDLINE=20206553; PubMed=10742094;

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RA Escaya A., MacDonald B.T., Meisler M.H., Baulac S., Huberfeld G.,
RA An-Gourfinkel I., Brice A., LeGuern E., Moulden B., Chagny D.,
RA Buresi C., Malafosse A.;
RT "Mutations of SCN1A, encoding a neuronal sodium channel, in two
RT families with GFS+2."
RL Nat. Genet. 24:343-345(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Jeong S.-Y., Goto J., Kanazawa I.;
RT "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
RT SCN1A."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA Sugawara T., Mazaki E.M., Yamakawa K.;
RT "Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
RT mRNA."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT THR-1067.
RA Ouchida M., Ohmori I.;
RT "Isoforms of human sodium channel SCN1A gene."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1335-1428 FROM N.A.
RX MEDLINE=94340991; PubMed=8062593;
RA Malo M.S., Blanchard B.J., Andresen J.M., Srivastava K., Chen X.N.,
RA Li X., Jabs E.W., Korenberg J.R., Ingram V.M.;
RT "Localization of a putative human brain sodium channel gene (SCN1A) to
RT chromosome band 2q24."
RL Cytogenet. Cell Genet. 67:178-186(1994).
RN [6]
RP SEQUENCE OF 1518-1940 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92275082; PubMed=1317301;
RA Lu C.-M., Han J., Rado T.A., Brown G.B.;
RT "Differential expression of two sodium channel subtypes in human
RT brain."
RL FEBS Lett. 303:53-58(1992).
RN [7]
RP VARIANTS GFS+2 VAL-188; LEU-1353 AND MET-1656.
RX MEDLINE=21152274; PubMed=11254444;
RA Wallace R.H., Scheffer I.E., Barnett S., Richards M., Dibbens L.,
RA Desai R.R., Lerman-Sagie T., Lev D., Kramidioti G., Gardner A.,
RA Ben-Zeev B., Goltzman I., Singh R., Mulley J.C., Berkovic S.F.;
RA Sutherland G.R., George A.L. Jr., Mulley J.C., Berkovic S.F.;
RT "Neuronal sodium-channel alpha1-subunit mutations in generalized
RT epilepsy with febrile seizures plus."
RL Am. J. Hum. Genet. 68:859-865(2001).
RN [8]
RP VARIANT GFS+2 ARG-1204.
RX MEDLINE=21152275; PubMed=11254445;
RA Escaya A., Heils A., MacDonald B.T., Haug K., Sander T., Meisler M.H.;
RT "A novel SCN1A mutation associated with generalized epilepsy with
RT febrile seizures plus -- and prevalence of variants in patients with
RT epilepsy."
RL Am. J. Hum. Genet. 68:866-873(2001).
RN [9]
RP VARIANT SMEI PHE-986.
RX MEDLINE=21257503; PubMed=11359211;
RA Claes L., Del-Favero J., Ceulemans B., Lagae L., Van Broeckhoven C.,
RA De Jonghe P.;
RT "De novo mutations in the sodium-channel gene SCN1A cause severe
RT myoclonic epilepsy of infancy."
RL Am. J. Hum. Genet. 68:1327-1332(2001).
RN [10]
RP VARIANT GFS+2 THR-1270.
RX MEDLINE=21630138; PubMed=11756608;
RA Abou-Khalil B., Ge Q., Desai R., Ryther R., Bazyk A., Bailey R.,
RA Haines J.L., Sutcliffe J.S., George A.L. Jr.;
RT "Partial and generalized epilepsy with febrile seizures plus and a
RT novel SCN1A mutation."

```

RL Neurology 57:2265-2272(2001).
 CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
 CC of excitable membranes. Assuming opened or closed conformations in
 CC response to the voltage difference across the membrane, the
 CC protein forms a sodium-selective channel through which Na(+) ions
 CC may pass in accordance with their electrochemical gradient.
 CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
 CC 3 smaller ones. This sequence represents a large polypeptide.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: Integral membrane protein.
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P35498-1; Sequence=Dieplayed;
 CC Name=2;
 CC IsoId=P35498-2; Sequence=VSP_001031;
 CC Note=No experimental confirmation available;
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- DISEASE: Defects in SCN1A are the cause of generalized epilepsy
 CC with febrile seizures plus type 2 (GEFS+2) [MTM:604233]. This
 CC autosomal dominant disorder is characterized by febrile seizures
 CC in children and afebrile seizures in adults. Penetrance is
 CC incomplete and a large intrafamilial variability of the phenotype
 CC is observed.
 CC -1- DISEASE: Defects in SCN1A are a cause of severe myoclonic epilepsy
 CC in infancy (SMEI) [MTM:607208], a severe form of generalized
 CC epilepsy with febrile seizures. SMEI is a rare disorder
 CC characterized by normal development before onset, seizures
 CC beginning in the first year of life in the form of generalized or
 CC unilateral febrile clonic seizures, secondary appearance of
 CC myoclonic seizures, and occasionally partial seizures. It is
 CC associated with ataxia, slowed psychomotor development, and mental
 CC decline.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC -----
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 CC -----
 DR EMBL; AF225985; AAK00217.1; -;
 DR EMBL; AY043484; AAK95360.1; -;
 DR EMBL; AB093548; BAC21101.1; -;
 DR EMBL; AB093549; BAC21102.1; -;
 DR EMBL; S71446; AAB31605.1; -;
 DR EMBL; X65362; CAA46439.1; -;
 DR EMBL; M91803; -; NOT_ANNOTATED_CDS.
 DR PIR; I52964; I52964.
 DR PIR; S29184; S29184.
 DR HSSP; P04775; 1BRY.
 DR GeneW; HGNC:10585; SCN1A.
 DR MIM; 182389; -;
 DR MIM; 604233; -;
 DR MIM; 607208; -;
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
 DR GO; GO:0006814; P:sodium ion transport; NAS.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR001696; Na_channel1.
 DR InterPro; IPR008051; Na_channel1.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans; 4.

DR Pfam; PF00612; IQ; 1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR PRINTS; PR01664; NACHANNEL1.
 DR PROSITE; PS50096; IQ; FALSE_NEG.
 DR Alternative splicing; Disease mutation; Epilepsy; Glycoprotein;
 DR Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat;
 DR Sodium channel; Transmembrane; Voltage-gated channel.
 FT REPEAT 110 454
 FT REPEAT 750 1022
 FT REPEAT 1200 1022
 FT REPEAT 1200 1514
 FT REPEAT 1523 1621
 FT REPEAT 124 147
 FT TRANSMEM 156 175
 FT TRANSMEM 189 207
 FT TRANSMEM 214 233
 FT TRANSMEM 230 273
 FT TRANSMEM 400 425
 FT TRANSMEM 763 787
 FT TRANSMEM 799 822
 FT TRANSMEM 831 850
 FT TRANSMEM 857 876
 FT TRANSMEM 893 913
 FT TRANSMEM 967 992
 FT TRANSMEM 1214 1237
 FT TRANSMEM 1251 1276
 FT TRANSMEM 1283 1304
 FT TRANSMEM 1309 1330
 FT TRANSMEM 1350 1377
 FT TRANSMEM 1457 1483
 FT TRANSMEM 1537 1560
 FT TRANSMEM 1572 1595
 FT TRANSMEM 1602 1625
 FT TRANSMEM 1636 1657
 FT TRANSMEM 1673 1695
 FT TRANSMEM 1762 1786
 FT CARBOHYD 211 211
 N-linked (GlcNAc...) (Potential).
 Query Match 100.0%; Score 28; DB 1; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 5.5e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MYLFFVPIIFGSPFTLNLFIGVITIDNF 28
 Db 1459 MYLFFVPIIFGSPFTLNLFIGVITIDNF 1486
 RESULT 18
 CINI_RAT
 ID CINI_RAT STANDARD; PRT; 2009 AA.
 AC P04774;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel protein type I alpha subunit (Voltage-gated sodium
 DE channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
 DE subunit).
 GN Name=Scn1a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=86146901; PubMed=3754035;
 RA Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kuraaki M.,
 RA "Takehashi H., Numa S.;
 RL Nature 320:188-192(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=87311395; PubMed=2442385;
 RA Noda M., Numa S.;

RT "Structure and function of sodium channel.";
 CC J. Receptor. Res. 7:467-497(1987).
 CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
 CC of excitable membranes. Assuming opened or closed conformations in
 CC response to the voltage difference across the membrane, the
 CC protein forms a sodium-selective channel through which Na(+) ions
 CC may pass in accordance with their electrochemical gradient.
 CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
 CC 3 smaller ones. This sequence represents a large polypeptide.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1, S2, S3, S5, S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC -----
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 CC -----
 DR EMBL; X03638; CAA27286.1; -;
 DR EMBL; M2253; AAA79965.1; -;
 DR PIR; A25019; A25019.
 DR HSSP; P04775; 1BXY.
 DR RGD; 69364; Scn1a.
 DR InterPro; IPR001682; Ca/Na pore.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR000048; IQ region.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR001686; Na channel_nlg.
 DR InterPro; IPR008051; Na channel.
 DR InterPro; IPR010526; Na trans_assoc.
 DR Pfam; PF00520; Ion_trans; 4.
 DR Pfam; PF00612; IQ; 1.
 DR Pfam; PF06512; Na trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR PRINTS; PR01664; NACHANNEL.
 DR PROSITE; PS50096; IQ; FALSE_NEG.
 KW Glycoprotein; Ion transport; Ionic channel; Multigene family; Repeat;
 KW Sodium channel; Transmembrane; Voltage-gated channel.
 FT REPEAT 110 454
 FT REPEAT 750 1022
 FT REPEAT 1200 1514
 FT REPEAT 1523 1821
 FT TRANSMEM 124 147
 FT TRANSMEM 156 175
 FT TRANSMEM 189 207
 FT TRANSMEM 214 233
 FT TRANSMEM 250 273
 FT TRANSMEM 400 425
 FT TRANSMEM 763 787
 FT TRANSMEM 799 822
 FT TRANSMEM 831 850
 FT TRANSMEM 857 876
 FT TRANSMEM 893 913
 FT TRANSMEM 967 992
 FT TRANSMEM 1214 1237
 FT TRANSMEM 1251 1276
 FT TRANSMEM 1283 1304
 FT TRANSMEM 1309 1330
 FT TRANSMEM 1350 1377
 FT TRANSMEM 1457 1483
 FT TRANSMEM 1537 1560
 FT TRANSMEM 1572 1595
 FT TRANSMEM 1602 1625
 FT TRANSMEM 1636 1657
 S4 of repeat IV.

FT TRANSMEM 1673 1695 S5 of repeat IV.
 FT TRANSMEM 1762 1786 S6 of repeat IV.
 FT CARBOHYD 211 211 N-linked (GlcNAc...)
 FT CARBOHYD 284 284 N-linked (GlcNAc...)
 FT CARBOHYD 295 295 N-linked (GlcNAc...)
 FT CARBOHYD 301 301 N-linked (GlcNAc...)
 FT CARBOHYD 306 306 N-linked (GlcNAc...)
 FT CARBOHYD 338 338 N-linked (GlcNAc...)
 FT CARBOHYD 601 601 N-linked (GlcNAc...)
 FT CARBOHYD 621 621 N-linked (GlcNAc...)
 FT CARBOHYD 681 681 N-linked (GlcNAc...)
 FT CARBOHYD 882 882 N-linked (GlcNAc...)
 FT CARBOHYD 1060 1060 N-linked (GlcNAc...)
 FT CARBOHYD 1064 1064 N-linked (GlcNAc...)
 FT CARBOHYD 1080 1080 N-linked (GlcNAc...)
 FT CARBOHYD 1146 1146 N-linked (GlcNAc...)
 FT CARBOHYD 1378 1378 N-linked (GlcNAc...)
 FT CARBOHYD 1392 1392 N-linked (GlcNAc...)
 FT CARBOHYD 1403 1403 N-linked (GlcNAc...)
 SQ SEQUENCE 2009 AA; 228769 MW; 6808466F6368373B CRC64;

Query Match 100.0%; Score 28; DB 1; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 5.5e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLYFYVFIIFGSPFTLNIFGVINDF 28
 Db 1459 MYLYFYVFIIFGSPFTLNIFGVINDF 1486

RESULT 19
 ID 090230 PRELIMINARY; PRT; 718 AA.
 AC 090230;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Sodium channel 1 (Fragment).
 OS Sternopygus macrurus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Gymnotiformes;
 OC Sternopygidae; Sternopygus.
 OX NCBI_TaxId=77841;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21310016; PubMed=11416226;
 RA Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
 RT Wilcox T.P., Zakon H.H.;
 RL "Evolution and divergence of sodium channel genes in vertebrates."; *Proc. Natl. Acad. Sci. U.S.A.* 98:7588-7592(2001).
 DR EMBL; AF378139; AAK55437.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005261; C:ion channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR InterPro; IPR001682; Ca/Na pore.
 DR InterPro; IPR002111; Cat channel_TrpL.
 DR InterPro; IPR005821; Ion trans.
 DR InterPro; IPR005820; M-channel_nlg.
 DR InterPro; IPR010526; Na trans_assoc.
 DR Pfam; PF00520; Ion_trans; 2.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 FT NON_TER 1 1
 FT NON_TER 718 718
 SQ SEQUENCE 718 AA; 81545 MW; 67C779B99DA3BCE CRC64;

Query Match 89.3%; Score 25; DB 2; Length 718;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YFYVFIIFGSPFTLNIFGVINDF 28
 Db 644 YFYVFIIFGSPFTLNIFGVINDF 668

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RESULT 20
O90226 PRELIMINARY; PRT; 743 AA.
ID O90226;
AC O90226;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
OS Sodium channel 5 (Fragment).
OC Sternoptygus macrurus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Gymnotiformes;
OC Sternopygidae; Sternopygus.
NCBI_TaxID=77841;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21310016; PubMed=11416226;
RA Lopreato G.F., Lu Y., Southwell A., Atkinson N.S., Hillis D.M.,
RA Wilcox T.P., Zakon H.H.;
RT "Evolution and divergence of sodium channel genes in vertebrates.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:7588-7592(2001).
DR EMBL; AF378143; AAK5441.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 2.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR Ion_transport; Ion_channel; Transmembrane; Transport.
KW NON_TER
FT NON_TER 1
SQ SEQUENCE 743 AA; 84781 MW; F2429665544CAB0C CRC64;

Query Match 89.3%; Score 25; DB 2; Length 743;
Best Local Similarity 100.0%; Pred. No. 2,36-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YFVIFIFGSFPTLNLFIVGIIDNF 28
DB 669 YFVIFIFGSFPTLNLFIVGIIDNF 693

RESULT 21
O91BFL PRELIMINARY; PRT; 1880 AA.
ID O91BFL;
AC O91BFL;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
OS Voltage-gated sodium channel.
OC Takifugu pardalis (puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
NCBI_TaxID=98921;
RN [1]
SEQUENCE FROM N.A.
RX TISSUE=Skletal muscle;
RX MEDLINE=20090650; PubMed=10623632;
RA Yocsu-Yamashita M., Nishimori K., Nitani Y., Isemura M., Sugimoto A.,
RA Yasumoto T.;
RT "Binding properties of 3H-PbTx-3 and 3H-saxitoxin to brain membranes
and to skeletal muscle membranes of puffer fish Takifugu pardalis, and the
primary structure of a voltage-gated Na+ channel alpha-subunit (fknai)
from skeletal muscle of F. pardalis.";
RL Biochem. Biophys. Res. Commun. 267:403-412(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

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CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AB030482; BAA30398.1; -.
DR HSSP; P04775; 1BYX.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR010526; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS50096; IQ; 1.
KW Ion_transport; Ion_channel; Sodium_channel; Transmembrane;
KW Transport; Voltage-gated_channel.
SQ SEQUENCE 1880 AA; 212084 MW; 4064836C3D43E02 CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1880;
Best Local Similarity 100.0%; Pred. No. 4,86-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 YFVIFIFGSFPTLNLFIVGIIDNF 28
DB 1302 YFVIFIFGSFPTLNLFIVGIIDNF 1326

RESULT 22
O9DF53 PRELIMINARY; PRT; 1949 AA.
ID O9DF53;
AC O9DF53;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
OS Sodium channel protein Scn8a.
GN Name=scn8a;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=oregon;
RA Tsai C.-W., Tseng J.-J., Horng J.-F., Wu J.-L., Tsay H.-J.;
RL Submitted (ABG-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AF297658; AAG18440.1; -.
DR HSSP; P04775; 1BYX.
DR ZFIN; ZDB-GENE-000828-1; scn8a.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR010526; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.

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DR Pfam; PF00612; IQ, 1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR PRINTS; PRO1667; NACHANNEL8.
 DR SMART; SM00015; IQ, 1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 1949 AA; 221760 MW; 68CA69664B0C7BC3 CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1949;
 Best Local Similarity 100.0%; Pred. No. 4.9e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 4 YFVIFIFGSPFTLNLFIVGIIDNF 28
 Db 1412 YFVIFIFGSPFTLNLFIVGIIDNF 1436

RESULT 23
 ID 075RX9 PRELIMINARY; PRT; 1962 AA.
 AC 075RX9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE TTX-resistant sodium channel splicing variant.
 GN Name=NAV1.5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ou S., Kameyama A., Kameyama M.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

RP [2]
 RA Ou S., Kameyama A., Kameyama M.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; AB158470; BAD12085.1;
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR010983; EF_Hand_like.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR008053; Na_channel5.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans; 4.
 DR Pfam; PF00612; IQ, 1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR PRINTS; PRO1666; NACHANNEL5.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 1962 AA; 221146 MW; 3EA3B3D897199C9A CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1962;
 Best Local Similarity 100.0%; Pred. No. 5e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 4 YFVIFIFGSPFTLNLFIVGIIDNF 28
 Db 1395 YFVIFIFGSPFTLNLFIVGIIDNF 1419

RESULT 24
 BAD12085 PRELIMINARY; PRT; 1962 AA.

AC BAD12085;
 DT 03-MAR-2004 (TrEMBLrel. 27, Created)
 DT 03-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 03-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE TTX-resistant sodium channel splicing variant.
 GN NAV1.5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ou S., Kameyama A., Kameyama M.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RA Ou S., Kameyama A., Kameyama M.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB158470; BAD12085.1; -.
 KW Ion channel.
 SQ SEQUENCE 1962 AA; 221146 MW; 3EA3B3D897199C9A CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1962;
 Best Local Similarity 100.0%; Pred. No. 5e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 4 YFVIFIFGSPFTLNLFIVGIIDNF 28
 Db 1395 YFVIFIFGSPFTLNLFIVGIIDNF 1419

RESULT 25
 ID 063541 PRELIMINARY; PRT; 1976 AA.
 AC 063541;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Sodium channel protein 6.
 GN Name=SCP6;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=95271284; PubMed=7751906;
 RA Schaller K.L., Krzemien D.M., Yarowsky P.J., Krueger B.K.,
 RA Caldwell J.H.;
 RT "A novel, abundant sodium channel expressed in neurons and glia.",
 RL J. Neurosci. 15:3231-3242 (1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; U39018; AAC42059.1; -.
 DR PIR; I56555; I56555;
 DR HSP; P04775; I8Y.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005241; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006814; P:cation ion transport; IEA.
 DR GO; GO:0006812; P:sodium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR000183; Decarboxylase.
 DR InterPro; IPR00048; Ion_trans.
 DR InterPro; IPR005821; M+channel_nlg.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR008054; Na_channel8.

DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans; 4.
 DR Pfam; PF00612; IQ; 1.
 DR PRINTS; PRO0170; Na_trans_assoc; 1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR SMART; SM00015; IQ; 1.
 DR PROSITE; PS00878; ODR_DC_2_1; UNKNOWN_1.
 DR PROSITE; PS00878; ODR_DC_2_1; UNKNOWN_1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 1976 AA; 225227 MW; B6949327A47FA88A CRC64;

Query Match 89.3%; Score 25; DB 2; Length 1976;
 Best Local Similarity 100.0%; Pred.No. 5e-16;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVIFIIFGSFTLNLFIGVIIDNP 28
 |||||
 DB 1439 YFVIFIIFGSFTLNLFIGVIIDNP 1463

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 Job time : 93.5 secs

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OW protein - protein search, using sw model

Run on: January 27, 2005, 17:36:50 ; Search time 22.5 Seconds
(without alignments)
82.529 Million cell updates/sec

Title: US-10-608-584-19

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Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

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Post-processing: Listing first 100 summaries

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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	# Match	Query Length	DB ID	Description
1	28	100.0	1836	4 US-10-162-012-24	Sequence 24, Appl
2	28	100.0	2005	3 US-08-836-325-7	Sequence 7, Appl
3	28	100.0	2005	4 US-09-457-571-7	Sequence 7, Appl
4	25	89.3	813	3 US-08-836-325-8	Sequence 8, Appl
5	25	89.3	813	4 US-09-457-571-8	Sequence 8, Appl
6	25	89.3	1011	3 US-08-836-325-2	Sequence 2, Appl
7	25	89.3	1011	4 US-09-457-571-2	Sequence 2, Appl
8	25	89.3	1976	3 US-09-024-020B-9	Sequence 9, Appl
9	25	89.3	1976	3 US-09-425-043-9	Sequence 9, Appl
10	25	89.3	1978	3 US-09-024-020B-3	Sequence 3, Appl
11	25	89.3	1978	3 US-09-425-043-3	Sequence 3, Appl
12	25	89.3	1984	3 US-08-836-325-10	Sequence 10, Appl
13	25	89.3	1984	4 US-09-457-571-10	Sequence 10, Appl
14	25	89.3	1988	3 US-09-024-020B-4	Sequence 4, Appl
15	25	89.3	1988	3 US-09-425-043-4	Sequence 4, Appl
16	25	89.3	1989	3 US-08-836-325-12	Sequence 12, Appl
17	25	89.3	1989	4 US-09-457-571-12	Sequence 12, Appl
18	25	89.3	2016	3 US-09-634-920-4	Sequence 4, Appl
19	25	89.3	2016	4 US-09-514-907A-2	Sequence 2, Appl
20	25	89.3	2016	4 US-09-896-994-2	Sequence 2, Appl
21	25	89.3	413	2 US-09-840-725-4	Sequence 4, Appl
22	21	75.0	413	2 US-08-808-793-25	Sequence 25, Appl
23	21	75.0	452	3 US-07-998-289B-6	Sequence 6, Appl
24	21	75.0	1233	4 US-09-354-147C-7	Sequence 7, Appl
25	21	75.0	1243	4 US-09-354-147C-8	Sequence 8, Appl
26	21	75.0	1765	4 US-09-354-147C-2	Sequence 2, Appl
27	21	75.0	1765	4 US-09-354-147C-3	Sequence 3, Appl

28	21	75.0	1765	4 US-09-354-147C-5	Sequence 5, Appl
29	21	75.0	1791	4 US-09-354-147C-42	Sequence 42, Appl
30	21	75.0	1820	3 US-07-998-289B-8	Sequence 8, Appl
31	21	75.0	1835	3 US-08-836-325-15	Sequence 15, Appl
32	21	75.0	1835	3 US-09-457-571-15	Sequence 15, Appl
33	21	75.0	1835	4 US-08-836-325-16	Sequence 16, Appl
34	21	75.0	1969	4 US-09-457-571-16	Sequence 16, Appl
35	21	75.0	1977	4 US-09-976-594-757	Sequence 757, App
36	21	75.0	1977	4 US-09-919-039-367	Sequence 367, App
37	21	75.0	1989	3 US-08-836-325-11	Sequence 11, Appl
38	21	75.0	1989	4 US-09-457-571-11	Sequence 11, Appl
39	21	75.0	2100	2 US-08-808-793-23	Sequence 23, Appl
40	21	75.0	2100	3 US-08-772-512A-19	Sequence 19, Appl
41	21	75.0	2104	2 US-08-808-793-4	Sequence 4, Appl
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43	21	75.0	2105	2 US-08-808-793-3	Sequence 3, Appl
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46	12	42.9	1956	3 US-09-527-013-10	Sequence 10, Appl
47	12	42.9	1956	4 US-08-836-325-6	Sequence 6, Appl
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53	7	25.0	310	3 US-08-605-284B-12	Sequence 12, Appl
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55	7	25.0	310	3 US-08-605-284B-14	Sequence 14, Appl
56	7	25.0	310	3 US-08-605-284B-15	Sequence 15, Appl
57	7	25.0	310	3 US-08-605-284B-16	Sequence 16, Appl
58	7	25.0	311	3 US-08-605-284B-18	Sequence 18, Appl
59	7	25.0	311	3 US-08-605-284B-13	Sequence 23, Appl
60	7	25.0	312	3 US-08-605-284B-20	Sequence 20, Appl
61	7	25.0	434	4 US-08-489-039A-13633	Sequence 13633, A
62	7	25.0	1956	3 US-08-843-417-2	Sequence 2, Appl
63	7	25.0	1956	4 US-09-527-013-2	Sequence 2, Appl
64	7	25.0	1957	4 US-08-669-656A-2	Sequence 2, Appl
65	7	25.0	1957	4 US-08-669-656A-8	Sequence 8, Appl
66	7	25.0	2132	4 US-08-669-656A-6	Sequence 6, Appl
67	6	21.4	22	1 US-08-103-445-12	Sequence 12, Appl
68	6	21.4	22	1 US-08-461-690B-12	Sequence 12, Appl
69	6	21.4	55	4 US-09-270-767-61121	Sequence 61121, A
70	6	21.4	63	4 US-09-328-352-4945	Sequence 4945, Ap
71	6	21.4	70	4 US-09-107-532A-4445	Sequence 4445, Ap
72	6	21.4	110	3 US-09-134-001C-5023	Sequence 5023, Ap
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76	6	21.4	180	4 US-09-270-767-38105	Sequence 38105, A
77	6	21.4	180	4 US-09-270-767-53322	Sequence 53322, A
78	6	21.4	237	4 US-09-538-032-332	Sequence 332, App
79	6	21.4	261	4 US-09-328-352-4430	Sequence 4430, App
80	6	21.4	262	4 US-09-489-039A-12430	Sequence 12430, A
81	6	21.4	267	4 US-09-543-681A-6127	Sequence 6127, Ap
82	6	21.4	274	4 US-09-134-000C-6450	Sequence 6450, Ap
83	6	21.4	298	3 US-09-134-001C-3631	Sequence 3631, Ap
84	6	21.4	316	2 US-08-846-762-9	Sequence 9, Appl
85	6	21.4	318	4 US-09-710-279-3118	Sequence 3118, Ap
86	6	21.4	322	3 US-09-134-001C-4064	Sequence 4064, Ap
87	6	21.4	326	4 US-09-107-532A-3665	Sequence 3665, Ap
88	6	21.4	337	4 US-09-252-991A-27966	Sequence 27966, A
89	6	21.4	342	4 US-09-543-681A-6588	Sequence 6588, Ap
90	6	21.4	342	4 US-09-489-039A-12502	Sequence 12502, A
91	6	21.4	359	4 US-09-328-352-7502	Sequence 7502, Ap
92	6	21.4	404	4 US-09-543-681A-6702	Sequence 6702, Ap
93	6	21.4	421	3 US-09-134-001C-4890	Sequence 4890, Ap
94	6	21.4	426	4 US-09-491-577-46	Sequence 46, Appl
95	6	21.4	430	4 US-09-489-039A-10587	Sequence 10587, A
96	6	21.4	495	4 US-09-275-252A-5	Sequence 5, Appl
97	6	21.4	528	2 US-08-527-152-2	Sequence 2, Appl
98	6	21.4	537	4 US-09-252-991A-20769	Sequence 20769, A
99	6	21.4	672	4 US-09-556-916-26	Sequence 26, Appl
100	6	21.4	672	4 US-09-556-916-28	Sequence 28, Appl

TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-457-571-7

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MYLVFVFIIFGSPFTLNLFGIVINDF 28
Db 1449 MYLVFVFIIFGSPFTLNLFGIVINDF 1476

RESULT 4
US-08-836-325-8
Sequence 8, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-325-8

Query Match 89.3%; Score 25; DB 3; Length 813;
Best Local Similarity 100.0%; Pred. No. 8.9e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YFVFIIFGSPFTLNLFGIVINDF 28
Db 347 YFVFIIFGSPFTLNLFGIVINDF 371

RESULT 5
US-09-457-571-8
Sequence 8, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-457-571-8

Query Match 89.3%; Score 25; DB 4; Length 813;
Best Local Similarity 100.0%; Pred. No. 8.9e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 YFVFIIFGSPFTLNFIGVITDNF 28
Db 347 YFVFIIFGSPFTLNFIGVITDNF 371

RESULT 6
US-08-836-325-2
Sequence 2, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational,
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1011 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-2

Query Match 89.3%; Score 25; DB 3; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 YFVFIIFGSPFTLNFIGVITDNF 28
Db 481 YFVFIIFGSPFTLNFIGVITDNF 505

RESULT 7
US-09-457-571-2
Sequence 2, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational,
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917, 0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1011 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-457-571-2

Query Match 89.3%; Score 25; DB 4; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1.1e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVFIIFGSPFTLNLFIVGIINDF 28
DB 481 YFVFIIFGSPFTLNLFIVGIINDF 505

RESULT 8
US-09-024-020B-9
Sequence 9, Application US/09024020B
Patent No. 6030810
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1976 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-020B-9

Query Match 89.3%; Score 25; DB 3; Length 1976;

Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVFIIFGSPFTLNLFIVGIINDF 28
DB 1439 YFVFIIFGSPFTLNLFIVGIINDF 1463

RESULT 9
US-09-425-043-9
Sequence 9, Application US/09425043
Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1976 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-425-043-9

Query Match 89.3%; Score 25; DB 3; Length 1976;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVFIIFGSPFTLNLFIVGIINDF 28
DB 1439 YFVFIIFGSPFTLNLFIVGIINDF 1463

RESULT 10
US-09-024-020B-3
Sequence 3, Application US/09024020B
Patent No. 6030810
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.

APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1978 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-020B-3

Query Match 89.3%; Score 25; DB 3; Length 1978;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVIFIIIGSFPTLNLFIGVIIDNF 28
DB 1441 YFVIFIIIGSFPTLNLFIGVIIDNF 1465

RESULT 11
US-09-425-043-3
Sequence 3, Application US/09425043
Patent No. 6335172
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425,043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/024,020
FILING DATE: 16-FEB-1998
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1978 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-425-043-3

Query Match 89.3%; Score 25; DB 3; Length 1978;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVIFIIIGSFPTLNLFIGVIIDNF 28
DB 1441 YFVIFIIIGSFPTLNLFIGVIIDNF 1465

RESULT 12
US-08-836-325-10
Sequence 10, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Thereof, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-10

Query Match 89.3%; Score 25; DB 3; Length 1984;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVIFIFGSPFTLNLFIGVINDF 28
Db 1434 YFVIFIFGSPFTLNLFIGVINDF 1458

RESULT 13
US-09-457-571-10
Sequence 10, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-457-571-10

Query Match 89.3%; Score 25; DB 4; Length 1984;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVIFIFGSPFTLNLFIGVINDF 28
Db 1434 YFVIFIFGSPFTLNLFIGVINDF 1458

RESULT 14
US-09-024-020B-4
Sequence 4, Application US/09024020B
Patent No. 6030810
GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERMAN, RONALD C.
TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
TITLE OF INVENTION: SODIUM CHANNEL 1-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: CA
COUNTRY: U.S.A.
ZIP: 94304-1397
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REFERENCE/DOCKET NUMBER: R0020B-REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-3097
TELEFAX: (650) 855-5322
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-020B-4

Query Match 89.3%; Score 25; DB 3; Length 1988;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVIFIFGSPFTLNLFIGVINDF 28

Db 1451 YFVIFIFGSPFTLNLFIGVIIDNF 1475

RESULT 15

US-09-425-043-4
; Sequence 4, Application US/09425043
; Patent No. 6335172
; GENERAL INFORMATION:
; APPLICANT: DELGADO, STEPHEN G.
; APPLICANT: DIETRICH, PAUL S.
; APPLICANT: RISH, LINDA M.
; APPLICANT: HERMAN, RONALD C.
; APPLICANT: SANGAMESWARAN, LAKSHMI
; TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE
; TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JANET PAULINE CLARK
; STREET: 3401 HILLVIEW AVENUE, MS A2-250
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94304-1397
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/425,043
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/024,020
; FILING DATE: 16-FEB-1998
; APPLICATION NUMBER: US 60/039,447
; FILING DATE: 26-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: R0020B-REG
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 852-3097
; TELEFAX: (650) 855-5322
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1988 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-425-043-4

Query Match 89.3%; Score 25; DB 3; Length 1988;

Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVIFIFGSPFTLNLFIGVIIDNF 28

Db 1451 YFVIFIFGSPFTLNLFIGVIIDNF 1475

RESULT 16

US-08-836-325-12
; Sequence 12, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational

; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1989 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-836-325-12

Query Match 89.3%; Score 25; DB 3; Length 1989;

Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YFVIFIFGSPFTLNLFIGVIIDNF 28

Db 1436 YFVIFIFGSPFTLNLFIGVIIDNF 1460

RESULT 17

US-09-457-571-12
; Sequence 12, Application US/09457571
; Patent No. 6703486
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,024003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-457-571-12

Query Match 89.3%; Score 25; DB 4; Length 1989;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YVVFIFGSGFTLNLFGVINDNF 28
Db 1436 YVVFIFGSGFTLNLFGVINDNF 1460

RESULT 18
US-09-634-920-4
Sequence 4, Application US/09634920
Patent No. 6342357
GENERAL INFORMATION:
APPLICANT: Splawski, Igor
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KYLQ1 AND
TITLE OF INVENTION: SCNSA AND METHODS FOR DETECTING SAME
FILE REFERENCE: 2323-155
CURRENT APPLICATION NUMBER: US/09/634,920
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/190,057
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/147,488
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 2016
TYPE: PRT
ORGANISM: Homo sapiens
US-09-634-920-4

Query Match 89.3%; Score 25; DB 3; Length 2016;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YVVFIFGSGFTLNLFGVINDNF 28
Db 1449 YVVFIFGSGFTLNLFGVINDNF 1473

RESULT 19
US-09-514-907A-2
Sequence 2, Application US/09514907A
Patent No. 6567705
GENERAL INFORMATION:
APPLICANT: Kenneth B. Stokes
Joa e Morissette
TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL
SENSING BY CARDIAC PACEMAKERS THROUGH
GENETIC TREATMENT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705xris LLP
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/514,907A
FILING DATE: 08-Feb-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul K. Legaard
REGISTRATION NUMBER: 38,534
REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-514-907A-2

Query Match 89.3%; Score 25; DB 4; Length 2016;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 YVVFIFGSGFTLNLFGVINDNF 28
Db 1449 YVVFIFGSGFTLNLFGVINDNF 1473

RESULT 20
US-09-696-994-2
Sequence 2, Application US/09896994
Patent No. 6665563
GENERAL INFORMATION:
APPLICANT: Ken Stokes
Joa e Morissette
TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563xris
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
STATE: PA

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; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/896,994
; FILING DATE: 02-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/514,907
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul K. Legard
; REGISTRATION NUMBER: 38,534
; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2016 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-896-994-2

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Query Match      89.3%; Score 25; DB 4; Length 2016;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 YFVIFIFGSPFTLNLFIVGIIDNF 28
DB      1449 YFVIFIFGSPFTLNLFIVGIIDNF 1473

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RESULT 21
US-09-840-125-4
; Sequence 4, Application US/09840125
; Patent No. 6787309
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
; FILE REFERENCE: 2323-155
; CURRENT APPLICATION NUMBER: US/09/840,125
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/634,920
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/147,488
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2016
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-125-4

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Query Match      89.3%; Score 25; DB 4; Length 2016;
Best Local Similarity 100.0%; Pred. No. 1.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 YFVIFIFGSPFTLNLFIVGIIDNF 28
DB      1449 YFVIFIFGSPFTLNLFIVGIIDNF 1473

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RESULT 22

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US-08-808-793-25
; Sequence 25, Application US/08808793
; Patent No. 5858713
; GENERAL INFORMATION:
; APPLICANT: Soderlund, David M.
; APPLICANT: Ingles, Patricia J.
; TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,793
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,361
; FILING DATE: 24-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,649
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-263-1636
; TELEFAX: 716-263-1600
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 413 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-793-25

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Query Match      75.0%; Score 21; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 5.9e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 FIFGSPFTLNLFIVGIIDNF 28
DB      94 FIFGSPFTLNLFIVGIIDNF 114

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RESULT 23
US-07-998-2898-6
; Sequence 6, Application US/079982898
; Patent No. 6027876
; GENERAL INFORMATION:
; APPLICANT: Black, Bruce C
; APPLICANT: Taylor, Martin
; APPLICANT: Heckel, David G
; TITLE OF INVENTION: Method for Monitoring Pesticide
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York

```

STATE: New York
COUNTRY: US
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998,289B
FILING DATE: 30-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/0A939
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-998-289B-6

Query Match 75.0%; Score 21; DB 3; Length 452;
Best Local Similarity 100.0%; Pred. No. 6.4e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FIIFGSFTLNLFIGVLIIDNF 28
DB 126 FIIFGSFTLNLFIGVLIIDNF 146

RESULT 24
US-09-354-147C-7
Sequence 7, Application US/09354147C
Patent No. 6573067
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 1233
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: (308)
OTHER INFORMATION: Xaa is leu. Xaa results from a "y" in SEQ ID NO: 6.
US-09-354-147C-7

Query Match 75.0%; Score 21; DB 4; Length 1233;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 FIIFGSFTLNLFIGVLIIDNF 28
FIIFGSFTLNLFIGVLIIDNF 28

DB 1092 FIIFGSFTLNLFIGVLIIDNF 1112

RESULT 25
US-09-354-147C-8
Sequence 8, Application US/09354147C
Patent No. 6573067
GENERAL INFORMATION:
APPLICANT: Dib-Hajj, Sulayman
TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
FILE REFERENCE: 44574-5004-01-US
CURRENT APPLICATION NUMBER: US/09/354,147C
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 60/072,990
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: US 60/109,402
PRIOR FILING DATE: 1998-11-20
PRIOR APPLICATION NUMBER: PCT/US99/02008
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 1243
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: partial human Nan amino acid seq.
US-09-354-147C-8

Query Match 75.0%; Score 21; DB 4; Length 1243;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 FIIFGSFTLNLFIGVLIIDNF 28
DB 1092 FIIFGSFTLNLFIGVLIIDNF 1112

Search completed: January 27, 2005, 17:54:19
Job time : 23.5 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:32:04 ; Search time 86.5 Seconds

(without alignments)
116.120 Million cell updates/sec

Title: US-10-608-584-29

Perfect score: 28

Sequence: 1 GIFFVSYIIISFLVVMNYAVILENF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2002273 seqs, 358729299 residues

Word size : 0
Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_23sep04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
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7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	100.0	405	4	AAm15136 Peptide #
2	28	100.0	405	4	ABb34128 Peptide #
3	28	100.0	405	4	AAm27591 Peptide #
4	28	100.0	405	4	ABb28960 Peptide #
5	28	100.0	405	4	ABb19569 Protein #
6	28	100.0	405	4	AAm67299 Human bon
7	28	100.0	405	4	AAm54918 Human bra
8	28	100.0	405	4	AAm56160 Human bra
9	28	100.0	405	4	ABg48961 Human liv
10	28	100.0	405	4	AAm02877 Peptide #
11	28	100.0	405	4	AAm04075 Peptide #
12	28	100.0	405	5	ABg36946 Human pep
13	28	100.0	1855	7	ADb78597 Human sod
14	28	100.0	1855	7	ADb78597 Human sod
15	28	100.0	1851	7	ADb78597 Human sod
16	28	100.0	1851	7	ADb78597 Human sod
17	28	100.0	1962	5	AAE20511 Human ion
18	28	100.0	1973	5	AAE20516 Human ion
19	28	100.0	1981	7	ABR83185 Human SCN
20	28	100.0	1998	5	AAE20510 Human ion
21	28	100.0	1998	7	ABR83184 Human SCN
22	28	100.0	1999	5	ABR80602 Human sod
23	28	100.0	2000	5	ABR80602 Human sod
24	28	100.0	2000	8	ADK81762 Human Nav
25	28	100.0	2005	4	AAb99676 Human adu

26	28	100.0	2005	4	AAb99677 Human neo
27	28	100.0	2009	4	AAb99674 Human adu
28	28	100.0	2009	5	AAE20515 Human ion
29	28	100.0	2009	5	ABg69292 Human sod
30	28	100.0	2009	5	ABg69291 Human sod
31	28	100.0	2009	5	ABg69293 Human sod
32	28	100.0	2009	5	ABg69289 Human sod
33	28	100.0	2009	5	ABg69290 Human sod
34	28	100.0	2009	5	ABg69290 Human sod
35	28	100.0	2009	5	ABg69290 Human sod
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37	28	100.0	2009	7	ADb78599 Human sod
38	28	100.0	2009	7	ADb78599 Human sod
39	28	100.0	2009	7	ADb78599 Human sod
40	28	100.0	2009	7	ADb78599 Human sod
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42	28	100.0	2009	7	ADb78599 Human sod
43	28	100.0	2009	7	ADb78599 Human sod
44	28	100.0	2009	7	ADb78599 Human sod
45	28	100.0	2009	7	ADb78599 Human sod
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47	28	100.0	2009	7	ADb78599 Human sod
48	28	100.0	2009	7	ADb78599 Human sod
49	28	100.0	2009	7	ADb78599 Human sod
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65	28	100.0	2009	7	ADb78599 Human sod
66	28	100.0	2009	7	ADb78599 Human sod
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68	28	100.0	2009	7	ADb78599 Human sod
69	28	100.0	2009	7	ADb78599 Human sod
70	28	100.0	2009	7	ADb78599 Human sod
71	28	100.0	2009	7	ADb78599 Human sod
72	28	100.0	2009	7	ADb78599 Human sod
73	28	100.0	2009	7	ADb78599 Human sod
74	28	100.0	2009	7	ADb78599 Human sod
75	28	100.0	2009	7	ADb78599 Human sod
76	28	100.0	2009	7	ADb78599 Human sod
77	28	100.0	2009	7	ADb78599 Human sod
78	28	100.0	2009	7	ADb78599 Human sod
79	28	100.0	2009	7	ADb78599 Human sod
80	28	100.0	2009	7	ADb78599 Human sod
81	28	100.0	2009	7	ADb78599 Human sod
82	28	100.0	2009	7	ADb78599 Human sod
83	28	100.0	2009	7	ADb78599 Human sod
84	28	100.0	2009	7	ADb78599 Human sod
85	28	100.0	2009	7	ADb78599 Human sod
86	28	100.0	2009	7	ADb78599 Human sod
87	28	100.0	2009	7	ADb78599 Human sod
88	28	100.0	2009	7	ADb78599 Human sod
89	28	100.0	2009	7	ADb78599 Human sod
90	28	100.0	2009	7	ADb78599 Human sod
91	28	100.0	2009	7	ADb78599 Human sod
92	28	100.0	2009	7	ADb78599 Human sod
93	28	100.0	2009	7	ADb78599 Human sod
94	28	100.0	2009	7	ADb78599 Human sod
95	28	100.0	2009	7	ADb78599 Human sod
96	28	100.0	2009	7	ADb78599 Human sod
97	28	100.0	2009	7	ADb78599 Human sod
98	28	100.0	2009	7	ADb78599 Human sod

99 13 46.4 1956 6 ABP72253
100 13 46.4 1956 6 ADA50144

Abp72253 Human PMS
Ada50144 Rat peritp

ALIGNMENTS

RESULT 1
ID AAM15136 standard; protein; 405 AA.
XX
AC AAM15136;
XX

DT 12-OCT-2001 (first entry)
XX

DE Peptide #1570 encoded by probe for measuring cervical gene expression.
XX

KW Probe; human; microarray; gene expression; cervical epithelial cell;
XX

OS Homo sapiens.
XX

PN WO200157278-A2.
XX

PD 09-AUG-2001.
XX

PF 30-JAN-2001; 2001WO-US000670.
XX

PR 04-FEB-2000; 2000US-0180312P.
XX

PR 26-MAY-2000; 2000US-0207456P.
XX

PR 30-JUN-2000; 2000US-00608408.
XX

PR 03-AUG-2000; 2000US-00632366.
XX

PR 21-SEP-2000; 2000US-0234687P.
XX

PR 27-SEP-2000; 2000US-0236359P.
XX

PR 04-OCT-2000; 2000GB-00024263.
XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX

DR WPI; 2001-488901/53.
XX

XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human cervical epithelial cells.

PT Claim 27; SEQ ID NO 19962; 487bp; English.
XX

PS The present invention relates to human single exon nucleic acid probes
XX (SENP; see AAI10068-AA128459). The present sequence is a peptide encoded
XX by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX can be used to produce a single exon microarray, which can be used for
XX measuring human gene expression in a sample derived from human cervical
XX epithelial cells. By measuring gene expression, the probes are therefore
XX useful in grading and/or staging of diseases of the cervix, notably
XX cervical cancer. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GIFFFVSYIIISFLVVMNYIAVILENF 28
|||
DB 158 GIFFFVSYIIISFLVVMNYIAVILENF 185

RESULT 2
ABB34128
ID ABB34128 standard; peptide; 405 AA.
XX

AC ABB34128;
XX
DT 04-FEB-2002 (first entry)
XX

DE Peptide #1634 encoded by human foetal liver single exon probe.
XX

KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX

OS Homo sapiens.
XX

PN WO200157277-A2.
XX

PD 09-AUG-2001.
XX

PF 30-JAN-2001; 2001WO-US000669.
XX

PR 04-FEB-2000; 2000US-0180312P.
XX

PR 26-MAY-2000; 2000US-0207456P.
XX

PR 30-JUN-2000; 2000US-00608408.
XX

PR 03-AUG-2000; 2000US-00632366.
XX

PR 21-SEP-2000; 2000US-0234687P.
XX

PR 27-SEP-2000; 2000US-0236359P.
XX

PR 04-OCT-2000; 2000GB-00024263.
XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX

DR WPI; 2001-483447/52.
XX

XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human fetal liver.

PT Claim 27; SEQ ID NO 26763; 639bp + Sequence listing; English.
XX

PS The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human foetal liver. The
XX present sequence is a peptide encoded by a single exon nucleic acid probe
XX of the invention. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GIFFFVSYIIISFLVVMNYIAVILENF 28
|||
DB 158 GIFFFVSYIIISFLVVMNYIAVILENF 185

RESULT 3
AAM27591
ID AAM27591 standard; protein; 405 AA.
XX
AC AAM27591;
XX

DT 17-OCT-2001 (first entry)
XX

DE Peptide #1628 encoded by probe for measuring placental gene expression.
XX

KW Probe; microarray; human; placenta; antenatal diagnosis;
XX

OS Homo sapiens.
XX

PN WO200157272-A2.
XX

PD 09-AUG-2001.
XX

XX 30-JAN-2001; 2001WO-US000663.
 PF 04-FEB-2000; 2000US-0180312P.
 XX 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488897/53.
 DR WPI; 2001-488897/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX
 PS Claim 27; SEQ ID NO 27860; 654bp; English.
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see A131315-A157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 XX
 SQ Sequence 405 AA;
 Query Match 100.0%; Score 28; DB 4; Length 405;
 Best Local Similarity 100.0%; Pred. No. 2.6e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GIFFVSYIIISFLVVMYIAVLENF 28
 Db 158 GIFFVSYIIISFLVVMYIAVLENF 185

RESULT 4
 ABB28960
 ID ABB28960 standard; peptide; 405 AA.
 XX
 AC ABB28960;
 XX
 DT 01-FEB-2002 (first entry)
 XX
 DE Peptide #1611 encoded by breast cell single exon nucleic acid probe.
 XX
 KW Human; microarray; single exon probe; gene expression; breast; disease;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157271-A2.
 PD 09-AUG-2001.
 PF 30-JAN-2001; 2001WO-US000662.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488897/53.
 XX

DR WPI; 2001-496933/54.
 XX
 XX New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.
 XX
 PS Claim 27; SEQ ID NO 11928; 327bp + Sequence Listing; English.
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a peptide
 CC encoded by a single exon nucleic acid probe of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 405 AA;
 Query Match 100.0%; Score 28; DB 4; Length 405;
 Best Local Similarity 100.0%; Pred. No. 2.6e-20;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GIFFVSYIIISFLVVMYIAVLENF 28
 Db 158 GIFFVSYIIISFLVVMYIAVLENF 185

RESULT 5
 ABB19569
 ID ABB19569 standard; protein; 405 AA.
 XX
 AC ABB19569;
 XX
 DT 23-JAN-2002 (first entry)
 XX
 DE Protein #1568 encoded by probe for measuring heart cell gene expression.
 XX
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157274-A2.
 PD 09-AUG-2001.
 PF 30-JAN-2001; 2001WO-US000666.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 PI WPI; 2001-488897/53.
 XX

XX Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 15; SEQ ID NO 21339; 530bp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting,
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease.
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
Db 158 GIFFVSYIIISFLVVMNYIAVILENF 185

RESULT 6
AAM67299
ID AAM67299 standard; protein; 405 AA.
XX
AC AAM67299;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 27605.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488900/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human bone marrow.
XX
PS Example 4; SEQ ID NO 27605; 658bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers
CC such as lymphoma, leukaemia and myeloma. The present sequence is a
CC protein encoded by one of the probes of the invention
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
Db 158 GIFFVSYIIISFLVVMNYIAVILENF 185

RESULT 7
AAM54918
ID AAM54918 standard; protein; 405 AA.
XX
AC AAM54918;
XX
DT 05-NOV-2001 (first entry)
XX
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27023.
XX
KW Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
OS Homo sapiens.
XX
PN WO200157275-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
PS Example 4; SEQ ID NO 27023; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 405 AA;

Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
Db 158 GIFFVSYIIISFLVVMNYIAVILENF 185


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RESULT 8
AAM56160
ID AAM56160 standard; protein; 405 AA.
XX
XX AAM56160;
AC
XX 05-NOV-2001 (first entry)
DT
XX
XX Human brain expressed single exon probe encoded protein SEQ ID NO: 28265.
DE
XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
XX
XX Homo sapiens.
OS
XX WO200157275-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000667.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-483446/52.
DR
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX
XX Example 4; SEQ ID NO 28265; 650bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
XX Sequence 405 AA;
SQ
Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 GIFFVSYIIISFLVVMNYTAVILENF 28
Db 158 GIFFVSYIIISFLVVMNYTAVILENF 185
RESULT 9
ABG48961
ID ABG48961 standard; peptide; 405 AA.
XX
XX ABG48961;
AC
XX 25-FEB-2003 (first entry)
DT
XX Human liver peptide, SEQ ID No 27609.
DE
XX Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX

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OS Homo sapiens.
XX
XX WO200157273-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000664.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488898/53.
DR
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human adult liver.
XX
XX Claim 27; SEQ ID NO 27609; 658bp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (1) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridizes at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (1) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG5930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 405 AA;
SQ
Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 GIFFVSYIIISFLVVMNYTAVILENF 28
Db 158 GIFFVSYIIISFLVVMNYTAVILENF 185
RESULT 10
AAM02877
ID AAM02877 standard; protein; 405 AA.
XX
XX AAM02877;
AC
XX 09-OCT-2001 (first entry)
DT
XX Peptide #1559 encoded by probe for measuring breast gene expression.
DE
XX Probe; human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
XX Homo sapiens.
OS
XX WO200157270-A2.
PN
XX 09-AUG-2001.
PD
XX 29-JAN-2001; 2001WO-US000661.
PF

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XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-0207456P.
PR 03-AUG-2000; 2000US-00608408.
PR 21-SEP-2000; 2000US-00632366.
PR 27-SEP-2000; 2000US-0234687P.
PR 04-OCT-2000; 2000US-0236359P.
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.
XX Claim 27; SEQ ID NO 11617; 322bp; English.
XX The present invention relates to novel single exon nucleic acid probes
XX (see AAI00010-AA110067). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for measuring human gene expression in
XX a human breast sample, where the probe hybridizes at high stringency to a
XX nucleic acid expressed in the human breast. The probes are useful for
XX predicting, diagnosing, grading, staging, monitoring and prognosing
XX diseases of the human breast, particularly those diseases with polygenic
XX etiology. The diseases include: breast cancer, disorders of development,
XX inflammatory diseases of the breast, fibrocystic changes, proliferative
XX breast disease and non-carcinoma tumours. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 405 AA;
Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFFFVSYYIIISFLVVMNYIAVLENF 28
DB 158 GIFFFVSYYIIISFLVVMNYIAVLENF 185
RESULT 11
ID AAM04075
XX AAM04075 standard; protein; 405 AA.
XX AC AAM04075;
XX DT 09-OCT-2001 (first entry)
XX DE Peptide #2757 encoded by probe for measuring breast gene expression.
XX KW Probe; human; breast disease; breast cancer; development disorder;
XX KM inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX OS Homo sapiens.
XX PN WO200157270-A2.
XX PD 09-AUG-2001.
XX PF 29-JAN-2001; 2001WO-US000661.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-0207456P.
XX PR 03-AUG-2000; 2000US-00608408.
XX PR 21-SEP-2000; 2000US-00632366.
XX PR 27-SEP-2000; 2000US-0234687P.
XX PR 04-OCT-2000; 2000US-0236359P.

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XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-476286/51.
XX Novel single exon nucleic acid probe used to measuring gene expression in
XX a human breast.
XX Claim 27; SEQ ID NO 12815; 322bp; English.
XX The present invention relates to novel single exon nucleic acid probes
XX (see AAI00010-AA110067). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for measuring human gene expression in
XX a human breast sample, where the probe hybridizes at high stringency to a
XX nucleic acid expressed in the human breast. The probes are useful for
XX predicting, diagnosing, grading, staging, monitoring and prognosing
XX diseases of the human breast, particularly those diseases with polygenic
XX etiology. The diseases include: breast cancer, disorders of development,
XX inflammatory diseases of the breast, fibrocystic changes, proliferative
XX breast disease and non-carcinoma tumours. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 405 AA;
Query Match 100.0%; Score 28; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFFFVSYYIIISFLVVMNYIAVLENF 28
DB 158 GIFFFVSYYIIISFLVVMNYIAVLENF 185
RESULT 12
ID ABG36946
XX ABG36946 standard; peptide; 405 AA.
XX AC ABG36946;
XX DT 19-AUG-2002 (first entry)
XX DE Human peptide encoded by genome-derived single exon probe SEQ ID 26611.
XX KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
XX KM chronic obstructive pulmonary disease; interstitial lung disease;
XX KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
XX KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
XX KW Hereditary-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
XX KW pulmonary alveolar proteinosis; lymphangioleiomyomatosis; Karsenger syndrome;
XX KW primary ciliary dyskinesia; fibrocystic pulmonary dysplasia;
XX KW hyaline membrane disease.
XX OS Homo sapiens.
XX PN WO200186003-A2.
XX PD 15-NOV-2001.
XX PF 30-JAN-2001; 2001WO-US000665.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000US-00024263.

```

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2002-114183/15.
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
XX Claim 27; SEQ ID NO 26611; 634pp; English.
XX
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karaganes syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
XX
XX Sequence 405 AA;
SQ
Query Match 100.0%; Score 28; DB 5; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
Db 158 GIFFVSYIIISFLVVMNYIAVILENF 185

KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW neurotropic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
XX Synthetic.
XX OS Homo sapiens.
XX PN WO2003008574-A1.
XX
XX 30-JAN-2003.
XX
XX 08-JUL-2002; 2002WO-AU000910.
XX
XX 18-JUL-2001; 2001AU-00006452.
XX PR 05-MAR-2002; 2002AU-00000910.
XX PR 13-MAY-2002; 2002AU-00002292.
XX
XX (BION-) BIONOMICS LTD.
XX (WALL-) WALLACE R W.
XX
XX Mulley JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
DR WPI; 2003-239332/23.
DR N-PSDB; ADB78636.
XX
XX Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
XX Claim 13; SEQ ID NO 141; 106pp; English.
XX
XX The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a CDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has neurotropic, neuroprotective, inotropic, antipyretic,
CC antiarrhythmic, antimigraine, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, neurotropic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonia, malignant hyperthermia,
CC myaethenia, cardiac arrhythmias, episodic ataxia, migraine, Alzheimer's
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 1855 AA;
SQ
Query Match 100.0%; Score 28; DB 7; Length 1855;
Best Local Similarity 100.0%; Pred. No. 1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
Db 1762 GIFFVSYIIISFLVVMNYIAVILENF 1789

RESULT 13
ADB78597
ID ADB78597 standard; protein; 1855 AA.
XX
XX ADB78597;
XX
XX 04-DEC-2003 (first entry)
XX
XX Human sodium channel subunit mutant SEQ ID NO:141.
XX
XX mutein; mutant; ion channel; ion channel subunit; ICS; neurotropic;
KW neuroprotective; inotropic; antipyretic; antiarrhythmic; antimigraine;

RESULT 14
ADB78607
ID ADB78607 standard; protein; 1950 AA.

XX ADB78607;
AC
XX
XX 04-DEC-2003 (first entry)
DT
XX
DE Human sodium channel subunit mutant SEQ ID NO:151.
XX
XX mutein; mutant; ion channel; ion channel subunit; ICS; noctropic;
KW neuroprotective; inotropic; antipruritic; antiarrhythmic; antiallergic;
KW antidepressant; antiparkinsonian; neuroleptic; tranquiliser; analgesic;
KW nephrotoxic; antidiabetic; ophthalmological; epilepsy;
KW ion channel dysfunction; human.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX WO2003008574-A1.
PN
XX
XX 30-JAN-2003.
PD
XX
XX 08-JUL-2002; 2002WO-AU000910.
PF
XX
XX 18-JUL-2001; 2001AU-00006452.
PR 05-MAR-2002; 2002AU-00000910.
PR 13-MAY-2002; 2002AU-00002292.
XX
XX (BION-) BIONOMICS LTD.
PA (WALL-) WALLACE R W.
XX
XX Muller JC, Harkin LA, Dibbens LM, Phillips HA, Heron SE;
PI Berkovic SF, Scheffer IE;
PI WPI; 2003-229332/23.
XX N-PSDB; ADB78646.
DR
XX
XX Identifying predisposition to an ion channel dysfunction, such as
PT periodic paralysis, cardiac arrhythmias, migraine, Alzheimer's disease,
PT schizophrenia, anxiety and depression, by detecting encoding-gene
PT mutation events.
XX
PS Claim 13; SEQ ID NO 151; 106pp; English.
XX
XX The invention relates to a novel method for identifying a subject
CC predisposed to a disorder associated with ion channel dysfunction. The
CC method comprises ascertaining if at least one of the genes encoding ion
CC channel subunits (ICS) has undergone a mutation event so that a cDNA
CC derived from the subject has any of 134 nucleotide sequences. The method
CC of the invention has noctropic, neuroprotective, inotropic, antipruritic,
CC antiarrhythmic, antiallergic, antidepressant, antiparkinsonian,
CC neuroleptic, tranquiliser, analgesic, nephrotoxic, antidiabetic, and
CC ophthalmological activity. A polynucleotide of the invention acts as an
CC ion channel agonist, or ion channel antagonist. The methods, isolated
CC nucleic acids, polypeptides, antibody, selective agonist, antagonist or
CC modulator of an ion channel, cells and genetically modified non-human
CC animal, are useful for the diagnosis and treatment of epilepsy and/or a
CC disorder associated with ion channel dysfunction, such as hyper- or hypo-
CC kalemic periodic paralysis, myotonia, malignant hyperthermia, and
CC myasthenia, cardiac arrhythmias, episodic ataxia, hyperthermia,
CC disease, Parkinson's disease, schizophrenia, hyperkplexia, anxiety,
CC depression, phobic obsessive symptoms, neuropathic pain, inflammatory
CC pain, chronic/acute pain, Bartter's syndrome, polycystic kidney disease,
CC Dent's disease, hyperinsulinaemic hypoglycaemia of infancy, cystic
CC fibrosis, congenital stationary night blindness and total colour
CC blindness. The present sequence represents a mutant protein of the
CC invention. The sequence data for this patent is not represented in the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 1950 AA;

Query March 100.0%; Score 28; DB 7; Length 1950;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIEFFVSYIIISFLVVMYIAVLENF 28
DB 1697 GIEFFVSYIIISFLVVMYIAVLENF 1724
RESULT 15
ADES9628
ID ADES9628 standard; protein, 1951 AA.
XX
XX ADES9628;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Rat Protein NP_037251, SEQ ID NO 5524.
DE
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
OS
XX
XX WO2003016475-A2.
PN
XX
XX 27-FEB-2003.
PD
XX
XX 14-AUG-2002; 2002WO-US025765.
PF
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
XX GENBANK; NP_037251.
DR
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT
XX
XX Claim 1; Page; 1017pp; English.
PS
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC polynucleotide, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 1951 AA;

QY 1 GIFFFVSYYIIISFLVVMNYIAVILENF 28
 DB 1751 GIFFFVSYYIIISFLVVMNYIAVILENF 1778

RESULT 18
 ID AAE20516 standard; protein; 1973 AA.
 AC AAE20516;
 DT 01-JUL-2002 (first entry)
 DE Human ion channel protein #7.
 KW Human; novel human protein; NHP; voltage-gated sodium channel;
 KW gene therapy; bioreactor; mental disorder; biological disorder;
 KW medical disorder.
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT Misc-difference 992 /note= "Encoded by MTG"
 FT Misc-difference 1067 /note= "Encoded by MTG"
 FT Misc-difference /note= "Encoded by RCA"
 PN WO200214498-A2.
 XX
 XX
 PD 21-FEB-2002.
 XX
 XX 15-AUG-2001; 2001WO-US025650.
 XX
 XX 16-AUG-2000; 2000US-0225989P.
 PR
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Turner CA, Mathur B, Mathur D;
 DR WPI; 2002-280757/32.
 DR N-PSDB; AAD32845.
 XX
 XX Novel polynucleotides encoding human sodium channel proteins,
 PT particularly voltage-gated sodium channel proteins useful for drug
 PT screening, diagnosis and in gene therapy of biological disorders.
 XX
 XX Claim 1; Page 64-68; 83pp; English.
 PS
 XX The present sequence is novel human protein (NHP), ion channel protein.
 CC NHP share structural similarity with mammalian sodium channel proteins,
 CC particularly voltage-gated sodium channel proteins. NHP oligonucleotides
 CC are useful as hybridisation probes for screening libraries and assessing
 CC gene expression patterns. Sequences derived from regions adjacent to the
 CC intron/exon boundaries of NHP gene can be used to design primers for use
 CC in amplification assays to detect mutations within the exons, splice
 CC sites, introns that can be used in diagnostics and pharmacogenomics. NHP
 CC nucleotide sequences are useful for drug screening effective in the
 CC treatment of symptomatic or phenotypic manifestations of perturbing the
 CC normal function of NHP in the body, and nucleotide constructs encoding the
 CC NHP products are useful to genetically engineer host cells to express NHP
 CC products in vivo. The present sequence represents a human NHP
 CC bioreactor in the body delivering a continuous supply of a NHP, a NHP
 CC peptide, or a NHP fusion protein to the body. Nucleotide construct
 CC encoding NHP products are also useful in gene therapy for modulating NHP
 CC expression and to produce genetically engineered host cells to express
 CC NHP products in vivo. NHP nucleotide sequences may also be used as part
 CC of ribozyme and/or triple helix sequences that are useful for NHP gene
 CC regulation. The NHP polypeptides are useful for generating antibodies, as
 CC reagents in diagnostic assays, for identifying other cellular gene
 CC products related to NHP and as reagents in assays for screening for
 CC compounds that are useful in the treatment of mental, biological or
 CC medical disorders and diseases

XX
 SQ Sequence 1973 AA;

Query Match 100.0%; Score 28; DB 5; Length 1973;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFFVSYYIIISFLVVMNYIAVILENF 28
 DB 1762 GIFFFVSYYIIISFLVVMNYIAVILENF 1789

RESULT 19

ID ABR83185 standard; protein; 1981 AA.

AC ABR83185;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 XX

DE Human SCN1A splice variant -84P:SCN1ADELP654-681.

KW SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic;
 KW neuroprotective; anesthetic; cyostatic; cerebroprotective; cardiac;
 KW hypotensive; gene therapy; human; splice variant.
 XX
 OS Homo sapiens.

PN WO2003072751-A2.
 XX
 XX 04-SEP-2003.
 PD
 XX 25-FEB-2003; 2003WO-US006010.
 PF
 XX 25-FEB-2002; 2002US-0359382P.
 PR
 XX (UTVA-) UNIV VANDERBILT.
 PA
 XX George AL, Lossin C;
 PI
 XX WPI; 2003-712725/67.
 DR N-PSDB; ACF57880.
 DR
 XX Recombinantly expressed sodium channel type 1 alpha subunit, useful in
 PT screening for modulators, for treating e.g. epilepsy.
 PT
 XX Disclosure; Page 162-169; 176pp; English.
 PS
 XX The invention relates to a recombinantly expressed and isolated human
 CC SCN1A (sodium channel type 1 alpha-subunit) (I). (II), optionally
 CC incorporated into a cell, is used to screen for specific modulators,
 CC potentially useful as anticonvulsant, antiepileptic, neuroprotective,
 CC analgesic and/or anesthetic agents, e.g. for treating severe myoclonic
 CC epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis,
 CC motor endplate diseases, hypertension, congestive heart failure and
 CC muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic
 CC and metastatic cancer cell lines). These activities can also be provided
 CC by gene therapy vectors that express (I) or the modulators. The
 CC modulators, also antibodies directed against (II), are used to detect
 CC SCN1A splice variant 84P:SCN1ADELP654-681
 CC
 XX Sequence 1981 AA;

SQ Sequence 1981 AA;

Query Match 100.0%; Score 28; DB 7; Length 1981;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFFVSYYIIISFLVVMNYIAVILENF 28
 DB 1734 GIFFFVSYYIIISFLVVMNYIAVILENF 1761

Query Match	Similarity	Score	DB	Length
Best Match	100.0%	100.0%	1.1e-19	1998
Matches	28	Conservative	0	Mismatches 0; Indels 0; Gaps 0

Oy	1	G I F F E V S Y I I I S F L V V V M N Y T A V I L E N F	28
Dd	1751	G I F F E V S Y I I I S F L V V V M N Y T A V I L E N F	1778
 RESULT 21			
ID	ABR83184	standard; protein; 1998 AA.	
AC	ABR83184;		
DT	15-JAN-2004	(first entry)	
DE	Human SCN1A splice variant -33P:SCN1ADELP671-681.		
KM	SCN1A; sodium channel type 1 alpha-subunit; anticonvulsant; analgesic; neuroprotective; anesthetic; cytostatic; cerebroprotective; cardiac; hypotensive; gene therapy; human; splice variant.		
OS	Homo sapiens.		
PX	WO2003072751-A2.		
PD	04-SEP-2003.		
PF	25-FEB-2003; 2003MO-US006010.		
PR	25-FEB-2002; 2002US-0359382P.		
PA	(UYVA-) UNIV VANDERBILT.		
PI	George AL, Lossin C;		
DR	WPI; 2003-712725/67.		
DR	N-PSDB; ACF57879.		
PT	Recombinantly expressed sodium channel type 1 alpha subunit, useful in screening for modulators, for treating e.g. epilepsy.		
PS	Disclosure; Page 148-156; 176pp; English.		
CC	The invention relates to a recombinantly expressed and isolated human SCN1A (sodium channel type 1 alpha-subunit) (I). (I), optionally incorporated into a cell, is used to screen for specific modulators, potentially useful as anticonvulsant, antiepileptic, neuroprotective, analgesic and/or anesthetic agents, e.g. for treating severe myoclonic epilepsy of infancy, stroke, cardiac arrest, hyperkalemic paralysis, motor encephalopathies, hypertension, congestive heart failure and muscular dystrophy also to treat cancer (SCN1A is expressed in prostatic and metastatic cancer cell lines). These activities can also be provided by gene therapy vectors that express (I) or the modulators. The modulators, also antibodies directed against (I), are used to detect sodium channel polypeptides. The present sequence represents a human SCN1A splice variant 33P:SCN1ADELP671-681 encoding cDNA		
SQ	Sequence 1998 AA:		
Query Match	100.0%;	Score 28;	DB 7; Length 1998;
Best Local Similarity	100.0%;	Pred. No. 1,le-19;	
Matches 28;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Oy	1	G I F F E V S Y I I I S F L V V V M N Y T A V I L E N F	28
Dd	1751	G I F F E V S Y I I I S F L V V V M N Y T A V I L E N F	1778
 RESULT 22			
ID	ABB06026	standard; protein; 1999 AA.	
AC	ABB06026;		
XX	ABB06026;		


```

DT 10-MAY-2002 (first entry)
XX
DE Human sodium channel SCN1A protein SEQ ID NO:2.
XX
KW Human; sodium channel; SCN1A; chromosome 2q24;
XX familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
OS Homo sapiens.
XX
XX WO200196552-A1.
XX
XX 20-DEC-2001.
XX
XX 12-JUN-2001; 2001WO-JP004956.
XX
XX 13-JUN-2000; 2000JP-00177540.
XX 13-JUN-2000; 2000JP-00177544.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Kanazawa I, Goto J, Jeong S;
XX
XX WPI; 2002-098066/13.
XX N-PSDB; ABL39689.
XX
XX Human sodium channels SCN1A and SCN3A and encoded genes, useful in
XX studying physiological mechanism in which excitant cells participate and
XX causes of diseases and developing drugs for motor endplate disease.
XX
XX Claim 1; Page 40-49; 88pp; Japanese.
XX
XX The present invention describes human sodium channels SCN1A and SCN3A.
XX The present sequence represents the human sodium channel SCN1A. SCN1A and
XX SCN3A have been located to the human chromosome 2 long arm, positions
XX 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
XX studying the physiological mechanism in which excitant cells participate
XX and cause human diseases, and in developing remedies for e.g. familial
XX hypercalcaemic periodic paralysis of extremities and motor endplate
XX disease
XX
XX Sequence 1999 AA;
XX
XX Query Match 100.0%; Score 28; DB 5; Length 1999;
XX Best Local Similarity 100.0%; Pred. No. 1,1e-19;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GIFFFVSYYIIISFLVVMNYIAVILENF 28
XX 1752 GIFFFVSYYIIISFLVVMNYIAVILENF 1779
XX
XX RESULT 23
XX ABB06027
XX ID ABB06027 standard; protein; 2000 AA.
XX
XX ABB06027;
XX
XX 10-MAY-2002 (first entry)
XX
XX Human sodium channel SCN3A protein SEQ ID NO:4.
XX
XX Human; sodium channel; SCN3A; chromosome 2q24-31;
XX familial hypercalcaemic periodic paralysis; motor endplate disease.
XX
XX Homo sapiens.
XX
XX WO200196552-A1.
XX
XX 20-DEC-2001.
XX
XX 12-JUN-2001; 2001WO-JP004956.
XX
XX 13-JUN-2000; 2000JP-00177540.
XX

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PR 13-JUN-2000; 2000JP-00177544.
XX
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX
XX Kanazawa I, Goto J, Jeong S;
XX
XX WPI; 2002-098066/13.
XX N-PSDB; ABL39690.
XX
XX Human sodium channels SCN1A and SCN3A and encoded genes, useful in
XX studying physiological mechanism in which excitant cells participate and
XX causes of diseases and developing drugs for motor endplate disease.
XX
XX Claim 2; Page 72-81; 88pp; Japanese.
XX
XX The present invention describes human sodium channels SCN1A and SCN3A.
XX The present sequence represents the human sodium channel SCN3A. SCN1A and
XX SCN3A have been located to the human chromosome 2 long arm, positions
XX 2q24 and 2q24-31 respectively. The sodium channel proteins are useful in
XX studying the physiological mechanism in which excitant cells participate
XX and cause human diseases, and in developing remedies for e.g. familial
XX hypercalcaemic periodic paralysis of extremities and motor endplate
XX disease
XX
XX Sequence 2000 AA;
XX
XX Query Match 100.0%; Score 28; DB 5; Length 2000;
XX Best Local Similarity 100.0%; Pred. No. 1,1e-19;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GIFFFVSYYIIISFLVVMNYIAVILENF 28
XX 1747 GIFFFVSYYIIISFLVVMNYIAVILENF 1774
XX
XX RESULT 24
XX ADK81762
XX ID ADK81762 standard; protein; 2000 AA.
XX
XX ADK81762;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human Nav1.3 protein.
XX
XX Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
XX diabetic neuropathy; arthritic pain; migraine headache;
XX infantile epilepsy; ataxia.
XX
XX Homo sapiens.
XX
XX WO2004016754-A2.
XX
XX 26-FEB-2004.
XX
XX 14-AUG-2003; 2003WO-US025465.
XX
XX 14-AUG-2002; 2002US-0403416P.
XX
XX (PHAA ) PHARMACIA CORP.
XX
XX Roberds SL;
XX
XX WPI; 2004-203785/19.
XX N-PSDB; ADK81761.
XX
XX New antisense compound targeted to a nucleic acid molecule encoding
XX Nav1.3, useful for treating a disease or condition associated
XX with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
XX disorder, or ataxia.
XX
XX Disclosure; SEQ ID NO 9096; 417pp; English.
XX

```


CC The present invention relates to an antisense compound targeted to a
 CC nucleic acid molecule encoding Nav1.3, where the antisense compound
 CC specifically hybridizes with and inhibits the expression of Nav1.3. The
 CC compound and composition are useful for treating a disease or condition
 CC associated with Nav1.3, e.g. pain including but not limited to
 CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
 CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
 CC pain from burns, migraine headache, cluster headache, mild-to-moderate
 CC headache; seizure disorder such as childhood seizure disorder, including
 CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
 CC sequence represents human Nav1.3 protein.

XX
 SQ Sequence 2000 AA;

Query Match 100.0%; Score 28; DB 8; Length 2000;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYYIIISFLVVMNYIAVILENF 28
 |||||
 Db 1747 GIFFFVSYYIIISFLVVMNYIAVILENF 1774

RESULT 25

AAB99676
 ID AAB99676 standard; protein; 2005 AA.

XX AAB99676;
 XX

DT 04-SEP-2001 (first entry)
 XX

DE Human adult form of SCN2A protein sequence SEQ ID NO:35.
 XX

Human; epilepsy; chromosome 2; SCN1A; SCN2A; SCN3A; identification;
 KM diagnosis; mutation; chromosome 2q23-q31; neurological disorder;
 KM anticonvulsant; neuroprotective.
 XX

OS Homo sapiens.
 XX

PN W0200138564-A2.
 XX

PD 31-MAY-2001.
 XX

PF 24-NOV-2000; 2000MO-CA001404.
 XX

PR 26-NOV-1999; 99US-0167623P.
 XX

PA (UTMC-) UNIV MCGILL.
 XX

PI Rouleau GA, Lafreniere RG, Rochefort D, Cossette P, Ragsdale D;
 XX

DR WPI; 2001-355945/37.
 XX

DR N-PSDB; AAH55793.
 XX

PT Determining a predisposition to epilepsy and/or development of epilepsy
 PT comprises determining the genotype of SCN1A, SCN2A and/or SCN3A, or a DNA
 PT variant, equivalent, or mutation which shows a linkage disequilibrium.
 XX

PS Disclosure; Page 123-130; 268pp; English.
 XX

CC The present invention describes a method (M1) of determining an
 CC individual's predisposition to epilepsy and/or development of epilepsy,
 CC as well as predicting the individual's response to medication. The method
 CC comprises determining the genotype of at least one gene selected from
 CC SCN1A, SCN2A or SCN3A, or a DNA variant, equivalent, or mutation which
 CC shows a linkage disequilibrium. SCN1A, SCN2A and SCN3A are all sodium
 CC channel genes located on chromosome 2. The idiopathic generalised
 CC epilepsy (IGE) gene is more specifically localised on chromosome 2q23-
 CC q31. Compounds identified as modulators of the biological activity of
 CC SCN1A, SCN2A or SCN3A proteins or genes, are useful for treating epilepsy
 CC or other neurological disorders. They have anticonvulsant and
 CC neuroprotective activities. AAH55763 to AAH56164 and AAB99674 to AAB99679
 CC represent SCN1A, SCN2A, and SCN3A cDNAs, gene fragments, PCR primers,

CC oligonucleotides and proteins given in the exemplification of the present
 CC invention
 XX
 SQ Sequence 2005 AA;

Query Match 100.0%; Score 28; DB 4; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYYIIISFLVVMNYIAVILENF 28
 |||||
 Db 1752 GIFFFVSYYIIISFLVVMNYIAVILENF 1779

Search completed: January 27, 2005, 17:45:18
 Job time : 88.5 secs

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GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: January 27, 2005, 17:36:05 ; Search time 17 Seconds
(without alignments)
158.475 Million cell updates/sec

Title: US-10-608-584-29

Perfect score: 28
Sequence: 1 GIFFFVSyllISFLVVMNYAVILENF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	303	2 S29185	sodium channel pro
2	28	100.0	423	2 S29184	sodium channel pro
3	28	100.0	1951	2 S00320	sodium channel pro
4	28	100.0	1983	2 A60054	sodium channel pro
5	28	100.0	2005	2 B25019	sodium channel pro
6	28	100.0	2009	2 A25019	sodium channel pro
7	24	85.7	1977	2 S54771	sodium channel pro
8	20	71.4	70	2 I59194	sodium channel pro
9	17	60.7	1993	2 T30902	sodium channel pro
10	16	57.1	2005	2 A46269	sodium channel pro
11	14	50.0	324	2 A45752	sodium channel pro
12	14	50.0	1976	2 I56555	sodium channel pro
13	13	46.4	1765	2 T42388	sodium channel pro
14	13	46.4	1957	2 S68453	sodium channel pro
15	12	42.9	1699	2 T31340	voltage-gated sodi
16	11	39.3	1522	2 JC1101	sodium channel pro
17	11	39.3	1695	2 J60084	voltage-gated sodi
18	11	39.3	1739	2 A48298	sodium channel pro
19	11	39.3	1784	2 T43167	sodium channel pro
20	11	39.3	1820	1 CHEE	sodium channel pro
21	10	35.7	213	2 A30302	sodium channel pro
22	10	35.7	428	2 S35215	sodium channel pro
23	10	35.7	1689	2 S72467	sodium channel pro
24	10	35.7	1820	2 A33299	sodium channel pro
25	10	35.7	2108	2 S72458	sodium channel pro
26	8	28.6	1835	2 I54323	sodium channel pro
27	8	28.6	1836	2 I64893	sodium channel pro
28	8	28.6	1836	2 JS0648	sodium channel pro
29	8	28.6	1836	2 I51964	sodium channel pro

30	8	28.6	1840	1 CHRTM1	sodium channel pro
31	7	25.0	79	2 G82709	hypothetical prote
32	7	25.0	675	2 B75036	hypothetical prote
33	7	25.0	2016	2 A38195	sodium channel pro
34	7	25.0	2019	2 A33996	sodium channel pro
35	7	25.0	2049	2 T43161	sodium channel pro
36	6	21.4	20	2 T26748	hypothetical prote
37	6	21.4	77	2 D64041	hypothetical prote
38	6	21.4	88	2 T17785	hypothetical prote
39	6	21.4	120	2 S62764	NADH2 dehydrogen
40	6	21.4	122	2 F71180	hypothetical prote
41	6	21.4	161	2 B96537	hypothetical prote
42	6	21.4	171	2 S55958	probable membrane
43	6	21.4	181	2 A87367	transcription regu
44	6	21.4	197	2 D86856	hypothetical prote
45	6	21.4	206	2 B71821	hypothetical prote
46	6	21.4	206	2 T01312	hypothetical prote
47	6	21.4	226	2 G95247	hypothetical prote
48	6	21.4	231	2 S12124	probable heme-bind
49	6	21.4	246	2 D98112	hypothetical prote
50	6	21.4	259	2 A13223	hypothetical prote
51	6	21.4	262	2 S53078	conserved hypothet
52	6	21.4	269	2 F97327	nitroreductase fam
53	6	21.4	274	2 I50682	tenascin - chicken
54	6	21.4	277	2 E75187	sugar abc transpor
55	6	21.4	317	2 B83039	probable permease
56	6	21.4	317	2 H97240	amino acid transp
57	6	21.4	331	2 H96020	hypothetical prote
58	6	21.4	341	2 T28798	hypothetical prote
59	6	21.4	341	2 E83737	C4-dicarboxylate t
60	6	21.4	370	1 XNVKUD	UDPglucose-hexose-
61	6	21.4	371	2 S75778	oligopeptide trans
62	6	21.4	374	2 T25943	hypothetical prote
63	6	21.4	380	2 T11114	ubiquinol-cytochro
64	6	21.4	399	2 T21015	hypothetical prote
65	6	21.4	419	2 T07817	S-locus-specific g
66	6	21.4	431	2 AFI422	cellobiose phospho
67	6	21.4	444	2 I40417	glycerol-3-phospha
68	6	21.4	463	2 E81141	xanthine/uracil pe
69	6	21.4	465	2 C86911	probable cell-divi
70	6	21.4	465	2 T10012	probable cell divi
71	6	21.4	469	2 G70699	probable rodA prot
72	6	21.4	487	2 T27069	hypothetical prote
73	6	21.4	490	2 T32003	hypothetical prote
74	6	21.4	506	2 T23163	hypothetical prote
75	6	21.4	515	2 T03717	GTP-binding protei
76	6	21.4	533	2 A80146	probable Branched-
77	6	21.4	545	2 S59143	NADH2 dehydrogen
78	6	21.4	545	2 T01288	protein kinase F27
79	6	21.4	558	2 E70756	hypothetical glyci
80	6	21.4	589	2 H63691	two-component sens
81	6	21.4	627	2 S67257	proline transport
82	6	21.4	634	2 T33528	hypothetical prote
83	6	21.4	666	2 F90069	hypothetical prote
84	6	21.4	710	2 T00055	hypothetical prote
85	6	21.4	713	2 A81317	probable integral
86	6	21.4	862	2 C97343	hypothetical prote
87	6	21.4	939	2 S75908	hypothetical prote
88	6	21.4	1195	2 C87691	hypothetical prote
89	6	21.4	1341	2 T18301	latrophilin-2, sp1
90	6	21.4	1354	2 T18375	latrophilin-2 (sp1
91	6	21.4	1356	2 T18367	latrophilin-2 (sp1
92	6	21.4	1369	2 T18379	latrophilin-2 (sp1
93	6	21.4	1384	2 T18366	latrophilin-2, sp1
94	6	21.4	1397	2 T18377	latrophilin-2 (sp1
95	6	21.4	1399	2 T18370	latrophilin-2 (sp1
96	6	21.4	1407	2 T18381	latrophilin-2 (sp1
97	6	21.4	1412	2 T18380	latrophilin-2 (sp1
98	6	21.4	1420	2 T18385	latrophilin-2 (sp1
99	6	21.4	1422	2 T18383	latrophilin-2, sp1
100	6	21.4	1435	2 T18387	latrophilin-2 (sp1

ALIGNMENTS

RESULT 1

S29185

sodium channel protein II - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Aug-1999

C/Accession: S29185; S34777

R/Lu, C.M.; Han, J.; Rado, T.A.; Brown, G.B.

FEBS Lett. 303, 53-58, 1992

A/Title: Differential expression of two sodium channel subtypes in human brain.

A/Reference number: S29184; MUID:92275082; PMID:1317301

A/Accession: S29185

A/Molecule type: mRNA

A/Residues: 1-303 <LUC>

A/Cross-references: EMBL:X65361

R/Lu, C.; Han, J.; Rado, T.A.; Brown, G.B.

Submitted to the EMBL Data Library, April 1992

A/Reference number: S34777

A/Accession: S34777

A/Molecule type: mRNA

A/Residues: 8-251, 'N' <LUC>

A/Cross-references: EMBL:X65361; NID:936419; PIDN:CAA46438.1; PID:936420

C/Species: sodium channel protein

C/Keywords: duplication; sodium channel; transmembrane protein; voltage-gated ion channel

F/51-75/Domain: transmembrane #status predicted <TM>

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 303;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 51 GIFFVSYIIISFLVVMNYIAVILENF 78

RESULT 2

S29184

sodium channel protein I - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C/Accession: S29184

R/Lu, C.M.; Han, J.; Rado, T.A.; Brown, G.B.

FEBS Lett. 303, 53-58, 1992

A/Title: Differential expression of two sodium channel subtypes in human brain.

A/Reference number: S29184; MUID:92275082; PMID:1317301

A/Accession: S29184

A/Molecule type: mRNA

A/Residues: 1-423 <LUC>

A/Cross-references: UNIPROT:P35498; EMBL:X65362; NID:936417; PIDN:CAA46439.1; PID:936418

C/Species: sodium channel protein

C/Keywords: duplication; sodium channel; transmembrane protein; voltage-gated ion channel

F/55-78/Domain: transmembrane #status predicted <TM1>

F/85-108/Domain: transmembrane #status predicted <TM1>

F/120-139/Domain: transmembrane #status predicted <TM3>

F/156-178/Domain: transmembrane #status predicted <TM4>

F/245-269/Domain: transmembrane #status predicted <TM5>

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 423;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 245 GIFFVSYIIISFLVVMNYIAVILENF 272

RESULT 3

S00320

sodium channel protein III - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C/Accession: S00320

R/Kayano, T.; Noda, M.; Flockerzi, V.; Takahashi, H.; Numa, S.

FEBS Lett. 228, 187-194, 1988

A/Title: Primary structure of rat brain sodium channel III deduced from the cDNA sequ

A/Reference number: S00320; MUID:88137594; PMID:2443363

A/Accession: S00320

A/Molecule type: mRNA

A/Residues: 1-1951 <KAY>

A/Cross-references: UNIPROT:P08104; EMBL:X00766; NID:957210; PIDN:CAA68735.1; PID:9572

A/Note: 270-11e, 278-1e, 355-1e, 513-1e, and 1059-Arg were also found

C/Species: sodium channel protein

C/Keywords: duplication; transmembrane protein

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 1951;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1698 GIFFVSYIIISFLVVMNYIAVILENF 1725

RESULT 4

A60054

sodium channel protein IIb, long form - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004

C/Accession: A60054; B44824

R/Johe, R.H.; Moorman, J.R.; Vandongen, A.M.J.; Kirsch, G.E.; Silberberg, H.; Schuster,

Brain Res. Mol. Brain Res. 7, 105-113, 1990

A/Title: Toxin and kinetic profile of rat brain type IIR sodium channels expressed in X

A/Reference number: A60054; MUID:90251117; PMID:2160038

A/Accession: A60054

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-1963 <JOH>

A/Cross-references: UNIPROT:Q64243

R/Schaller, K.L.; Krizemien, D.M.; McKenna, N.M.; Caldwell, J.H.

J. Neurosci. 12, 1370-1381, 1992

A/Title: Alternatively spliced sodium channel transcripts in brain and muscle.

A/Reference number: A44824; MUID:92211397; PMID:1313493

A/Accession: B44824

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 611-662 <SCH>

A/Cross-references: GB:S97388; NID:9248225; PIDN:AA821984.1; PID:9248226

A/Experimental source: skeletal muscle

A/Note: sequence inconsistent with the nucleotide translation

C/Species: sodium channel protein

C/Keywords: duplication; glycoprotein; ion transport; sodium channel; transmembrane prot

Query Match

Best Local Similarity 100.0%; Score 28; DB 2; Length 1983;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1730 GIFFVSYIIISFLVVMNYIAVILENF 1757

RESULT 5

B25019

sodium channel protein II - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004

C/Accession: B25019; S24804

R/Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, F

Nature 320, 188-192, 1986

A/Title: Existence of distinct sodium channel messenger RNAs in rat brain.

```

A:Reference number: A93377; MUID:86146901; PMID:3754035
A:Accession: B25019
A:Molecule type: mRNA
A:Residues: 1-2005 <NOD>
A:Cross-references: UNIPROT:Q63509
A:Experimental source: brain
R:Sarao, R.; Gupta, S.K.; Auid, V.J.; Dunn, R.J.
submitted to the EMBL Data Library, August 1991
A:Description: Developmentally regulated RNA splicing of rat brain sodium channel mRNAs.
A:Reference number: S24803
A:Accession: S24804
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 183-188, 'D', 190-305 <SAR>
A:Cross-references: EMBL:X61149; NID:957074; PIDN:CAA43458.1; PID:957076
C:Superfamily: sodium channel protein
C:Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g
Query Match 100.0%; Score 28; DB 2; Length 2005;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
Db 1752 GIFFVSYIIISFLVVMNYIAVILENF 1779

RESULT 6
A25019
sodium channel protein I - rat
N:Alternate names: sodium channel protein A
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 03-Jul-2004
A:Accession: A25019; S40783; 184764
R:Noda, M.; Ikeda, T.; Kayano, T.; Suzuki, H.; Takeshima, H.; Kurasaki, M.; Takahashi, H
Nature 320, 188-192, 1986
A>Title: Existence of distinct sodium channel messenger RNAs in rat brain.
A:Reference number: A93377; MUID:86146901; PMID:3754035
A:Accession: A25019
A:Molecule type: mRNA
A:Residues: 1-2009 <NOD>
A:Cross-references: UNIPROT:P04774; GB:X03638; NID:957216; PIDN:CAA27286.1; PID:957217
A:Experimental source: brain
R:Sarao, R.; Gupta, S.K.; Auid, V.J.; Dunn, R.J.
Nucleic Acids Res. 19, 5673-5679, 1991
A>Title: Developmentally regulated alternative RNA splicing of rat brain sodium channel
A:Reference number: S40782; MUID:92051314; PMID:1658739
A:Accession: S40783
A:Molecule type: DNA
A:Residues: 177-253 <SAR>
R:Noda, M.; Numa, S.
J. Recept. Res. 7, 467-497, 1987
A>Title: Structure and function of sodium channel.
A:Reference number: I50536; MUID:87311395; PMID:2442385
A:Accession: 184764
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2009 <RES>
A:Cross-references: GB:M22253; NID:91041089; PIDN:AAA79965.1; PID:91041089
C:Superfamily: sodium channel protein
C:Keywords: duplication; ion transport; sodium channel; transmembrane protein; voltage-g
Query Match 100.0%; Score 28; DB 2; Length 2009;
Best Local Similarity 100.0%; Pred. No. 3.2e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
Db 1762 GIFFVSYIIISFLVVMNYIAVILENF 1789

RESULT 7
S54771

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```

sodium channel alpha subunit - human
C:Species: Homo sapiens (man)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C:Accession: S54771
R:Klugbauer, N.; Lacinova, L.; Flockerzi, V.; Hofmann, F.
EMBO J. 14, 1084-1090, 1995
A>Title: Structure and functional expression of a new member of the tetrodotoxin-sensitive
A:Reference number: S54771; MUID:95237189; PMID:7720699
A:Accession: S54771
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1977 <KLU>
A:Cross-references: UNIPROT:Q15858; EMBL:X82835; NID:9758109; PIDN:CAA58042.1; PID:97581
C:Superfamily: sodium channel protein
C:Keywords: duplication
Query Match 85.7%; Score 24; DB 2; Length 1977;
Best Local Similarity 100.0%; Pred. No. 3.4e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 FVSYIIISFLVVMNYIAVILENF 28
Db 1729 FVSYIIISFLVVMNYIAVILENF 1752

RESULT 8
I59194
sodium channel protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Nov-1997
C:Accession: I59194
R:Han, J.; Lu, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 335-339, 1991
A>Title: Direct amplification of a single dissected chromosomal segment by polymerase ch
A:Reference number: I59194; MUID:9110524; PMID:1846440
A:Accession: I59194
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-70 <RES>
A:Cross-references: GB:M55662; NID:9179560; PID:9553206
C:Superfamily: sodium channel protein
C:Keywords: duplication
Query Match 71.4%; Score 20; DB 2; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.3e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GIFFVSYIIISFLVVMNY 20
Db 51 GIFFVSYIIISFLVVMNY 70

RESULT 9
T30902
sodium channel SCAP1 alpha chain - California sea hare
C:Species: Aplysia californica (California sea hare)
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30902
R:Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.
DNA Cell Biol. 16, 347-356, 1997
A>Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.
A:Reference number: Z20929; MUID:97238630; PMID:9115644
A:Accession: T30902
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1993 <DYB>
A:Cross-references: UNIPROT:P90670; EMBL:U66915; NID:91842248; PID:91842249; PIDN:AA474
C:Superfamily: sodium channel protein
Query Match 60.7%; Score 17; DB 2; Length 1993;
Best Local Similarity 100.0%; Pred. No. 3.7e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 12 SFLVVMNYIAVILENF 28
 |||||
 Db 1719 SFLVVMNYIAVILENF 1735

RESULT 10

A46269
 sodium channel alpha chain HBA - human
 C:Species: Homo sapiens (man)
 C>Date: 20-Oct-1993 #sequence_revision 18-Nov-1994 #text_change 21-Nov-1997
 C:Accession: A46269
 R:Ahmed, C.M.; Ware, D.H.; Lee, S.C.; Pattem, C.D.; Ferrer-Montiel, A.V.; Schinder, A.F.
 Proc. Natl. Acad. Sci. U.S.A. 89, 8220-8224, 1992
 A>Title: Primary structure, chromosomal localization, and functional expression of a vol
 A:Reference number: A46269; MUID:92390418; PMID:1325650
 A:Accession: A46269
 A:Molecule type: mRNA
 A:Residues: 1-2005 <AM>
 A:Cross-references: GB:M94055
 A:Experimental source: Brain
 A>Note: sequence extracted from NCBI backbone (NCBIP:113082)
 C:Genetics:
 A:Map position: 2q23-q24.3
 C:Superfamily: sodium channel protein
 C:Keywords: duplication

Query Match 57.1%; Score 16; DB 2; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 3.8e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFLV 16
 |||||
 Db 1752 GIFFFVSYIIISFLV 1767

RESULT 11

A45752
 sodium channel protein PCSC-1 - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jul-2004
 C:Accession: A45752
 R:Stillé, M.N.; Xu, Y.C.; Baracchini, E.; Goodman, R.H.; Cooperman, S.S.; Mandel, G.; Chi
 J. Clin. Invest. 84, 331-336, 1989
 A>Title: Expression of diverse Na(+) channel messenger RNAs in rat myocardium. Evidence
 A:Reference number: A45752; MUID:89292178; PMID:2544627
 A:Accession: A45752
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-324 <SL>
 A:Cross-references: UNIPROT:Q63360; GB:M27223; NID:g205611; PIDN:AAA1666.1; PID:g205612
 C:Superfamily: sodium channel protein
 C:Keywords: duplication

Query Match 50.0%; Score 14; DB 2; Length 324;
 Best Local Similarity 100.0%; Pred. No. 8.7e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFL 14
 |||||
 Db 86 GIFFFVSYIIISFL 99

RESULT 12

I56555
 sodium channel protein 6 - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I56555
 R:Schaller, K.L.; Krzymien, D.M.; Yarowsky, P.J.; Kueger, B.K.; Caldwell, J.H.
 J. Neurosci. 15, 3231-3242, 1995
 A>Title: A novel, abundant sodium channel expressed in neurons and glia.
 A:Reference number: I56555; MUID:95271284; PMID:7751906
 A:Accession: I56555

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1976 <RES>
 A:Cross-references: UNIPROT:Q63541; GB:IJ39018; NID:g829033; PIDN:AA42059.1; PID:g829034
 C:Genetics:
 A:Gene: SGP6
 C:Superfamily: sodium channel protein
 C:Keywords: duplication

Query Match 50.0%; Score 14; DB 2; Length 1976;
 Best Local Similarity 100.0%; Pred. No. 3.8e-06;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFFVSYIIISFL 14
 |||||
 Db 1738 GIFFFVSYIIISFL 1751

RESULT 13

T42388
 sodium channel alpha chain - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T42388
 R:DiB-Hajj, S.D.; Tytrell, L.; Black, J.A.; Waxman, S.G.
 Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998
 A>Title: Nav, a novel voltage-gated Na channel, is expressed preferentially in periphery
 A:Reference number: T22149; MUID:98338024; PMID:9671787
 A:Accession: T42388
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1765 <DIB>
 A:Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AA4
 A:Experimental source: strain Sprague-Dawley; dorsal root ganglia
 A>Note: preferentially expressed in sensory neurons within dorsal root ganglia and trig
 C:Superfamily: sodium channel protein

Query Match 46.4%; Score 13; DB 2; Length 1765;
 Best Local Similarity 100.0%; Pred. No. 3.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 VVMNYIAVILENF 28
 |||||
 Db 1575 VVMNYIAVILENF 1587

RESULT 14

S68453
 sodium channel protein SNS - rat
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: S68453
 R:Akopian, A.N.; Siviletti, L.; Wood, J.N.
 Nature 379, 257-262, 1996
 A>Title: A tetrodotoxin-resistant voltage-gated sodium channel expressed by sensory neur
 A:Reference number: S68453; MUID:96138382; PMID:8538791
 A:Accession: S68453
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1957 <AKO>
 A:Cross-references: UNIPROT:Q63554; GB:X92184; NID:g1209466; PIDN:CAA63095.1; PID:g12094
 A:Experimental source: dorsal root ganglia
 C:Superfamily: sodium channel protein
 C:Keywords: sodium channel; transmembrane protein; voltage-gated ion channel
 F:132-148/Domain: transmembrane #status predicted <TM1>
 F:158-174/Domain: transmembrane #status predicted <TM2>
 F:225-241/Domain: transmembrane #status predicted <TM3>
 F:249-265/Domain: transmembrane #status predicted <TM4>
 F:316-392/Domain: transmembrane #status predicted <TM5>
 F:666-682/Domain: transmembrane #status predicted <TM6>
 F:702-718/Domain: transmembrane #status predicted <TM7>
 F:731-747/Domain: transmembrane #status predicted <TM8>
 F:788-804/Domain: transmembrane #status predicted <TM9>

F:865-881/Domain: transmembrane #status predicted <TM10>
 F:1156-1172/Domain: transmembrane #status predicted <TM11>
 F:1194-1210/Domain: transmembrane #status predicted <TM12>
 F:1221-1237/Domain: transmembrane #status predicted <TM13>
 F:1286-1302/Domain: transmembrane #status predicted <TM14>
 F:1400-1416/Domain: transmembrane #status predicted <TM15>
 F:1482-1498/Domain: transmembrane #status predicted <TM16>
 F:1516-1532/Domain: transmembrane #status predicted <TM17>
 F:1546-1562/Domain: transmembrane #status predicted <TM18>
 F:1606-1622/Domain: transmembrane #status predicted <TM19>
 F:1708-1724/Domain: transmembrane #status predicted <TM20>

Query Match 46.4%; Score 13; DB 2; Length 1957;
 Best Local Similarity 100.0%; Pred. No. 3.8e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 VNMVIAVILENF 28
 Db 1715 VNMVIAVILENF 1727

RESULT 15
 T31340
 voltage-gated sodium channel homolog - Bdeiloura candida
 C:Species: Bdeiloura candida
 C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
 C:Accession: T31340
 R:Jelioski, M.C.; Greenberg, R.M.; Anderson, P.A.
 submitted to the EMBL Data Library, March 1997
 A:Description: A putative voltage-gated sodium channel from the turbellarian flatworm Bd
 A:Reference number: 221006
 A:Accession: T31340
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1699 <E2>
 A:Cross-references: UNIPROT:O02037; EMBL:U93074; NID:g1947093; PID:g1947094; PIDN:AAC630
 A:Genetics:
 A:Gene: Na1
 C:Superfamily: sodium channel protein

Query Match 42.9%; Score 12; DB 2; Length 1699;
 Best Local Similarity 100.0%; Pred. No. 0.00035;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 VNMVIAVILENF 28
 Db 1536 VNMVIAVILENF 1547

RESULT 16
 JC1101
 sodium channel protein - Bleeker's squid
 C:Species: Loligo bleekeri (Bleeker's squid)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
 C:Accession: JC1101
 R:Sato, C.; Matsunoto, G.
 Biochem. Biophys. Res. Commun. 186, 61-68, 1992
 A:Title: Primary structure of squid sodium channel deduced from the complementary DNA se
 A:Reference number: JC1101; MUID:92337659; PMID:1339273
 A:Accession: JC1101
 A:Molecule type: mRNA
 A:Residues: 1-1522 <S2>
 A:Cross-references: UNIPROT:Q05973; GB:D14525; NID:G287448; PID:G287449
 C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
 C:Keywords: phosphoprotein; sodium channel; transmembrane protein; voltage-gated ion cha
 F:51-70/Domain: transmembrane #status predicted <TM1>
 F:78-100/Domain: transmembrane #status predicted <TM2>
 F:113-134/Domain: transmembrane #status predicted <TM3>
 F:144-167/Domain: transmembrane #status predicted <TM4>
 F:180-201/Domain: transmembrane #status predicted <TM5>
 F:309-331/Domain: transmembrane #status predicted <TM6>
 F:407-426/Domain: transmembrane #status predicted <TM7>
 F:443-464/Domain: transmembrane #status predicted <TM8>

F:473-491/Domain: transmembrane #status predicted <TM9>
 F:499-522/Domain: transmembrane #status predicted <TM10>
 F:532-553/Domain: transmembrane #status predicted <TM11>
 F:605-626/Domain: transmembrane #status predicted <TM12>
 F:778-797/Domain: transmembrane #status predicted <TM13>
 F:816-837/Domain: transmembrane #status predicted <TM14>
 F:847-868/Domain: transmembrane #status predicted <TM15>
 F:875-898/Domain: transmembrane #status predicted <TM16>
 F:916-937/Domain: transmembrane #status predicted <TM17>
 F:1010-1032/Domain: transmembrane #status predicted <TM18>
 F:1101-1120/Domain: transmembrane #status predicted <TM19>
 F:1133-1154/Domain: transmembrane #status predicted <TM20>
 F:1163-1184/Domain: transmembrane #status predicted <TM21>
 F:1195-1218/Domain: transmembrane #status predicted <TM22>
 F:1237-1258/Domain: transmembrane #status predicted <TM23>
 F:1324-1346/Domain: transmembrane #status predicted <TM24>

Query Match 39.3%; Score 11; DB 2; Length 1522;
 Best Local Similarity 100.0%; Pred. No. 0.0032;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NNMVIAVILENF 28
 Db 1344 NNMVIAVILENF 1354

RESULT 17
 JE0084
 voltage-gated sodium channel alpha subunit - hydromedusa (Polyorchis penicillatus)
 N:Alternate names: PpSCN 1
 C:Species: Polyorchis penicillatus
 C:Date: 11-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
 A:Accession: JE0084
 R:Spafford, J.D.; Spencer, A.N.; Gallin, W.J.
 Biochem. Biophys. Res. Commun. 244, 772-780, 1998
 A:Title: A putative voltage-gated sodium channel alpha subunit (PpSCN1) from the hydrozo
 A:Reference number: JE0084; MUID:98205797; PMID:9535741
 A:Accession: JE0084
 A:Molecule type: mRNA
 A:Residues: 1-1695 <SPA>
 A:Cross-references: UNIPROT:O62604; GB:AF047380; NID:G3005563; PIDN:AAC38974.1; PID:G300
 A:Comment: This protein is the only pore-forming alpha subunit available to account for
 C:Superfamily: sodium channel protein
 C:Keywords: glycoprotein
 F:201,273,299,584,1065,1082,1089,1428/Binding site: carbohydrate (Asn) (covalent) #statu

Query Match 39.3%; Score 11; DB 2; Length 1695;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NNMVIAVILENF 28
 Db 1463 NNMVIAVILENF 1473

RESULT 18
 A48298
 sodium channel homolog - jellyfish (Cyanea capillata)
 C:Species: Cyanea capillata
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 A:Accession: A48298
 R:Anderson, P.A.V.; Holman, M.A.; Greenberg, R.M.
 Proc. Natl. Acad. Sci. U.S.A. 90, 7419-7423, 1993
 A:Title: Deduced amino acid sequence of a putative sodium channel from the scyphozoan je
 A:Reference number: A48298; MUID:93348284; PMID:8394021
 A:Accession: A48298
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1739 <AND>
 A:Cross-references: UNIPROT:Q17314; GB:L15445
 A:Genetics:
 A:Gene: CYN1
 C:Superfamily: sodium channel protein

C/Keywords: transmembrane protein

Query Match 39.3%; Score 11; DB 2; Length 1739;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMVIAVILENF 28
Db 1517 NMVIAVILENF 1527

RESULT 19

T43167

sodium channel protein - California market squid

C/Species: Loligo opalescens (California market squid)

C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004

C/Accession: T43167

R/Rosenthal, J.J.; Gilly, W.F.

Proc. Natl. Acad. Sci. U.S.A. 90, 10026-10030, 1993

A/Title: Amino acid sequence of a putative sodium channel expressed in the giant axon of

A/Reference number: Z2324; MUID:94052096; PMID:8234251

A/Accession: T43167

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1784 <ROS>

A/Cross-references: UNIPROT:Q25377; EMBL:J19979; NID:g349118; PID:g349119; PIDN:AAA16202

A/Experimental source: stellate ganglia

C/Superfamily: sodium channel protein

C/Keywords: ion transport; membrane protein; sodium channel; voltage-gated ion channel

Query Match

Best Local Similarity 39.3%; Score 11; DB 2; Length 1784;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMVIAVILENF 28
Db 1582 NMVIAVILENF 1592

RESULT 20

CHRE

sodium channel protein - electric eel

C/Species: Electrophorus electricus (electric eel)

C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C/Accession: A03178; I50536

R/Noda, M.; Shimizu, S.; Tanabe, T.; Takai, T.; Kayano, T.; Ikeda, T.; Takahashi, H.; Na

da, H.; Miyata, T.; Numa, S.

Nature 312, 121-127, 1984

A/Title: Primary structure of Electrophorus electricus sodium channel deduced from cDNA

A/Reference number: A03178; MUID:85061498; PMID:6209577

A/Accession: A03178

A/Molecule type: mRNA

A/Residues: 1-1820 <NOD>

A/Cross-references: UNIPROT:P02719; GB:X01119; NID:g62776; PIDN:CAA25587.1; PID:g62777

R/Noda, M.; Numa, S.

J. Recept. Res. 7, 467-497, 1987

A/Title: Structure and function of sodium channel.

A/Reference number: I50536; MUID:87311395; PMID:2442385

A/Accession: I50536

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1820 <NOD>

A/Cross-references: GB:M2252; NID:G1041048; PIDN:AAA79960.1; PID:G1041049

C/Comment: This membrane glycoprotein mediates the voltage-dependent sodium-ion permeab

C/Comment: The protein forms a sodium-selective channel through which sodium ions

C/Comment: This sequence contains four highly homologous internal repeats (excluding res

C/Comment: The four repeating units are thought to be oriented pseudosymmetrically across

C/Comment: Available data suggest that activation and inactivation gates are located near

C/Superfamily: sodium channel protein

C/Keywords: duplication; glycoprotein; ion transport; membrane protein; sodium channel, v

F:111-419,555-807,989-1281,1311-1587/Region: duplication internal repeats I, II, III and

F:111-141,555-585,989-1019,1311-1341/Region: S1 of repeats I through IV

F:150-171,557-620,1033-1057,1353-1376/Region: S2 of repeats I through IV

F:177-197,626-643,1062-1079,1381-1398/Region: S3 of repeats I through IV

F:204-224,651-671,1092-1112,1417-1437/Region: S4 of repeats I through IV

F:244-264,691-711,1132-1152,1454-1474/Region: S5 of repeats I through IV

F:379-402,767-790,1236-1264,1544-1567/Region: S6 of repeats I through IV

F:205,278,288,317,591,690,797,1160,1174,1806/Binding site: carbohydrate (Asn) (covalent)

Query Match 39.3%; Score 11; DB 1; Length 1820;

Best Local Similarity 100.0%; Pred. No. 0.0037;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SELVNMVNYIA 22
Db 1554 SELVNMVNYIA 1564

RESULT 21

A30302

sodium channel protein P15 - fruit fly (Drosophila melanogaster) (fragment)

C/Species: Drosophila melanogaster

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 21-Nov-1997

C/Accession: A30302

R/Ramaswami, M.; Tanouye, M.A.

Proc. Natl. Acad. Sci. U.S.A. 86, 2079-2082, 1989

A/Title: Two sodium-channel genes in Drosophila: implications for channel diversity.

A/Reference number: A30302; MUID:89184571; PMID:2538830

A/Accession: A30302

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-213 <RAM>

C/Genetics:

A/Gene: FLYBase:NaCP60E

A/Cross-references: FLYBase:FBgn0002920

C/Superfamily: sodium channel protein

C/Keywords: duplication

Query Match 35.7%; Score 10; DB 2; Length 213;

Best Local Similarity 100.0%; Pred. No. 0.0065;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMVIAVILENF 27
Db 171 NMVIAVILENF 180

RESULT 22

S35215

sodium channel protein - house fly

C/Species: Musca domestica (house fly)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S35215

R/Milliamson, W.S.; Denholm, I.; Bell, C.A.; Devonshire, A.L.

Mol. Gen. Genet. 240, 17-22, 1993

A/Title: Knockdown resistance (kdr) to DDT and pyrethroid insecticides maps to a sodium

A/Reference number: S35215; MUID:93344154; PMID:8101963

A/Accession: S35215

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-428 <WIL>

A/Cross-references: UNIPROT:Q9TX80

C/Superfamily: sodium channel protein

C/Keywords: duplication

Query Match 35.7%; Score 10; DB 2; Length 428;

Best Local Similarity 100.0%; Pred. No. 0.011;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 NMVIAVILENF 27
Db 165 NMVIAVILENF 174

RESULT 23

S72467

sodium channel protein para-type alpha chain - German cockroach (strain CSMA) (fragment)
 C:Species: Blatella germanica (german cockroach)

A:Variety: strain CSMA

C:Date: 29-Jul-1997 #sequence _revision 29-Aug-1997 #text_change 09-Jul-2004

C:Accession: S72467, S72487

R:Miyauchi, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.

submitted to the EMBL Data Library, September 1996

A:Description: Cloning and sequencing of the para-type sodium channel gene from susceptible

A:Reference number: S72467

A:Accession: S72467

A:Molecule type: mRNA

A:Residues: 1-168 <MT>

R:Cross-references: UNIPROT:Q93135; EMBL:U71083; NID:gl633647; PIDN:ABB82037.1; PID:gl63

R:Miyauchi, M.; Ohyama, K.; Dunlap, D.Y.; Matsumura, F.

Mol. Gen. Genet. 252, 61-68, 1996

A:Title: Cloning and sequencing of the para-type sodium channel gene from susceptible an

A:Reference number: S72487, MUID:96397510, PMID:8804404

A:Accession: S72487

A:Molecule type: mRNA

A:Residues: 711-819 <MTW>

A:Cross-references: EMBL:U71083

C:Superfamily: sodium channel protein

C:Keywords: duplication; sodium channel; transmembrane protein

Query Match

Query Match 35.7%; Score 10; DB 2; Length 1689;
 Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NMVIAVILEN 27

DB 1614 NMVIAVILEN 1623

RESULT 24

A33299

sodium channel protein - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster

C:Date: 20-Dec-1989 #sequence _revision 20-Dec-1989 #text_change 21-Nov-1997

C:Accession: A33299

R:Loughney, K.; Kreber, R.; Ganetzky, B.

Cell 58, 1143-1154, 1989

A:Title: Molecular analysis of the para locus, a sodium channel gene in Drosophila.

A:Reference number: A33299; MUID:89376565; PMID:2550145

A:Accession: A33299

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1820 <LOU>

A:Cross-references: GB:M32078; GB:M24285

C:Genetics:

A:Gene: FlyBase:Para

A:Cross-references: FlyBase:FBgn0003036

C:Superfamily: sodium channel protein

C:Keywords: duplication; phosphoprotein; transmembrane protein

Query Match

Query Match 35.7%; Score 10; DB 2; Length 1820;
 Best Local Similarity 100.0%; Pred. No. 0.038;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NMVIAVILEN 27

DB 1809 NMVIAVILEN 1818

RESULT 25

S72458

sodium channel protein para-type alpha chain - house fly (strain Cooper)
 C:Species: Musca domestica (house fly)

A:Variety: strain Cooper

C:Date: 24-Oct-1998 #sequence _revision 24-Oct-1998 #text_change 09-Jul-2004

C:Accession: S72458

R:Williamson, M.S.; Martinez-Torres, D.; Hick, C.A.; Devonshire, A.L.

Mol. Gen. Genet. 252, 51-60, 1996

A:Title: Identification of mutations in the housefly para-type sodium channel gene assoc

A:Reference number: S72458; MUID:96397509; PMID:8804403

A:Accession: S72458

A:Molecule type: mRNA

A:Residues: 1-2108 <MTL>

A:Cross-references: UNIPROT:Q94615; EMBL:X96668

A:Experimental source: strain Cooper

C:Genetics:

A:Map position: 3

C:Superfamily: sodium channel protein

C:Keywords: alternative splicing; glycoprotein; phosphoprotein; sodium channel; transmem

F:302,314,332,967,1451,1470/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:541,1208,1582/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match

Query Match 35.7%; Score 10; DB 2; Length 2108;
 Best Local Similarity 100.0%; Pred. No. 0.042;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 NMVIAVILEN 27

DB 1841 NMVIAVILEN 1850

Search completed: January 27, 2005, 17:52:48

Job time : 19 secs

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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:35:20 ; Search time 92.5 Seconds
(without alignments)
174.167 Million cell updates/sec

Title: US-10-608-584-29
Perfect score: 28
Sequence: 1 GIFFVSYITISFLVVMNYAVILENF 28

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1825181 seqs, 575374646 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Uniprot_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	100.0	404	2 O8CCS4	O8CCS4 mus musculus
2	28	100.0	510	2 O62242	O62242 mus musculus
3	28	100.0	519	2 O9P2J1	O9P2J1 homo sapien
4	28	100.0	1951	1 C1N3_RAT	P08104 rattus norv
5	28	100.0	1951	2 O9C007	O9C007 homo sapien
6	28	100.0	1981	2 O8IUJ6	O8IUJ6 homo sapien
7	28	100.0	2000	1 C1N3_HUMAN	O9UJ46 homo sapien
8	28	100.0	2005	1 C1N2_HUMAN	O9J250 homo sapien
9	28	100.0	2005	1 C1N2_RAT	P04775 rattus norv
10	28	100.0	2007	2 O9YGN7	O9YGN7 cynops pyrr
11	28	100.0	2009	1 C1N1_HUMAN	P35498 homo sapien
12	28	100.0	2009	1 C1N1_RAT	P04774 rattus norv
13	27	96.4	253	2 O8CNI8	O8CNI8 mus musculus
14	27	85.7	309	2 O62205	O62205 mus musculus
15	24	85.7	1977	2 O15858	O15858 homo sapien
16	24	85.7	1984	2 O28644	O28644 Oryctolagus
17	24	85.7	1984	2 O08562	O08562 rattus norv
18	17	60.7	279	2 O54811	O54811 cavia porce
19	17	60.7	1993	2 P90670	P90670 alysia cal
20	16	57.1	1880	2 O91BFI	O91BFI takifugu pa
21	14	50.0	278	2 O54812	O54812 cavia porce
22	14	50.0	324	2 O63360	O63360 rattus norv
23	14	50.0	364	2 O9P2O6	O9P2O6 homo sapien
24	14	50.0	364	2 O9N2E3	O9N2E3 pongo pygma
25	14	50.0	364	2 O9N2E4	O9N2E4 gorilla gor
26	14	50.0	364	2 O9N2E5	O9N2E5 pan troglod
27	14	50.0	1976	2 O63541	O63541 rattus norv
28	14	50.0	1978	1 C1N8_MOUSE	O9WCU3 mus musculus
29	14	50.0	1978	2 O88420	O88420 rattus norv
30	14	50.0	1980	1 C1N8_HUMAN	O9UCD0 homo sapien
31	14	50.0	1988	2 O88421	O88421 rattus norv

32	13	46.4	523	2 O62243	O62243 mus musculus
33	13	46.4	1765	2 O88457	O88457 rattus norv
34	13	46.4	1765	2 O9JMD4	O9JMD4 mus musculus
35	13	46.4	1765	2 O9R053	O9R053 mus musculus
36	13	46.4	1791	2 O8NDX3	O8NDX3 homo sapien
37	13	46.4	1791	2 O9UHE0	O9UHE0 homo sapien
38	13	46.4	1791	2 O9UIJ3	O9UIJ3 homo sapien
39	13	46.4	1956	2 O9YSY9	O9YSY9 homo sapien
40	13	46.4	1956	2 O62968	O62968 rattus norv
41	13	46.4	1957	2 O601Y3	O601Y3 mus musculus
42	13	46.4	1957	2 O63554	O63554 rattus norv
43	13	46.4	1957	2 AAS45602	AAS45602 mus muscu
44	13	46.4	1958	2 P70276	P70276 mus musculus
45	13	46.4	1962	2 O46669	O46669 canis faml
46	12	42.9	46	2 O71A32	O71A32 sus scrofa
47	12	42.9	46	2 AAO11213	AAO11213 sus acro
48	12	42.9	1599	2 O02037	O02037 bdelioura c
49	11	39.3	1522	1 C1N1_LOBL	C1N1_LOBL
50	11	39.3	1695	2 O62604	O62604 polyorchis
51	11	39.3	1740	2 O17314	O17314 cyanea capi
52	11	39.3	1784	2 O25377	O25377 loligo opal
53	11	39.3	1820	1 C1N4_ELEEL	C1N4_ELEEL
54	10	35.7	428	2 O9TX80	O9TX80 musca domes
55	10	35.7	1089	2 O8IS97	O8IS97 varroa deat
56	10	35.7	1130	2 O9XZC1	O9XZC1 boophilus m
57	10	35.7	1347	2 O7PMT4	O7PMT4 anopheles g
58	10	35.7	1361	2 O7PMT0	O7PMT0 anopheles g
59	10	35.7	1689	2 O9J135	O9J135 blattella g
60	10	35.7	1695	2 O94584	O94584 heliothis v
61	10	35.7	2031	2 O01306	O01306 blattella g
62	10	35.7	2031	2 O01307	O01307 blattella g
63	10	35.7	2051	2 O86D17	O86D17 pediculus h
64	10	35.7	2051	2 O86D18	O86D18 pediculus h
65	10	35.7	2051	2 O86D19	O86D19 pediculus h
66	10	35.7	2058	2 O6DLT4	O6DLT4 aedes albop
67	10	35.7	2064	2 O6DLT3	O6DLT3 aedes aegypt
68	10	35.7	2086	2 O86M38	O86M38 pediculus h
69	10	35.7	2104	2 O25440	O25440 musca domes
70	10	35.7	2105	2 O25439	O25439 musca domes
71	10	35.7	2108	2 O94615	O94615 musca domes
72	10	35.7	2131	1 C1N4_DROME	C1N4_DROME
73	10	35.7	2215	2 O86D77	O86D77 varroa deat
74	8	28.6	487	2 O8AV15	O8AV15 gallus gall
75	8	28.6	1834	2 O28371	O28371 equus cabal
76	8	28.6	1836	1 C1N4_HUMAN	C1N4_HUMAN
77	8	28.6	1840	1 C1N4_RAT	C1N4_RAT
78	8	28.6	1840	2 O70611	O70611 rattus norv
79	8	28.6	1841	2 O9PER0	O9PER0 mus musculus
80	8	25.0	79	2 O9PE09	O9PE09 xyella fas
81	7	25.0	250	2 O96YL8	O96YL8 bruchydanio
82	7	25.0	397	2 O7ZVJ1	O7ZVJ1 bruchydanio
83	7	25.0	444	2 O7ZVU7	O7ZVU7 leprospira
84	7	25.0	444	2 O8FPG4	O8FPG4 leprospira
85	7	25.0	444	2 AAS68827	AAS68827 leprospira
86	7	25.0	616	2 O7QWH6	O7QWH6 giardia lam
87	7	25.0	640	1 PTMA_BUCBP	PTMA_BUCBP
88	7	25.0	649	2 O7ZSK6	O7ZSK6 leprospira
89	7	25.0	649	2 O8F303	O8F303 leprospira
90	7	25.0	656	2 AAS69976	AAS69976 leprospira
91	7	25.0	662	2 O81260	O81260 plasmodium
92	7	25.0	662	2 O8TU41	O8TU41 mechanosarc
93	7	25.0	678	2 O9UJ26	O9UJ26 pyrococcus
94	7	25.0	678	2 O6HCZ6	O6HCZ6 bacillus th
95	7	25.0	678	2 O81L64	O81L64 bacillus th
96	7	25.0	678	2 AAT33890	AAT33890 bacillus th
97	7	25.0	1394	2 O8H8L9	O8H8L9 oryza sativ
98	7	25.0	1717	2 O90519	O90519 fuqua rubrip
99	7	25.0	1949	2 O9DF53	O9DF53 brachydanio
100	7	25.0	1962	2 O75RX9	O75RX9 homo sapien

ALIGNMENTS

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RESULT 1
08CCS4 PRELIMINARY; PRT; 404 AA.
ID 08CCS4
AC 08CCS4
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:643040810 product:sodium channel protein II
DE homolog (Fragment).
GN Name:A230052E19Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN 2
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN 3
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN 4
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayata N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN 5
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076811;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kikunai T., Tachiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Harada M., Nishida T., Harada A.,
RA Yamamoto R., Matsuno H., Sakaguchi S., Ikegami T., Kasahagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN 6
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Adachi U., Aizawa K., Akiyama T., Arakawa T., Bono H., Carninci P.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiroka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

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RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AK032187; BAC27748.1; -.
DR MGD; MG1:2444703; A230052E19Rik.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat_channel_TrypL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ_1.
DR PROSITE; PS50096; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
FT NON TER 1
SQ SEQUENCE 404 AA; 45671 MW; C5ED26B0F080C09 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 404;
Best Local Similarity 100.0%; Pred. No. 28-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFVSYYIIISFLVVMYIAVLENF 28
Db 151 GIFFVSYYIIISFLVVMYIAVLENF 178

RESULT 2
062242 PRELIMINARY; PRT; 510 AA.
ID 062242
AC 062242
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Sodium channel (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Jover E., Shah V.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; L42341; AA67695.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006814; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat_channel_TrypL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR00170; NACHANNEL.

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DR SMART; SM00015; IQ; 1.
 DR PROSITE; PSS0096; IQ; 1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 FT NON_TER 510 510
 SQ SEQUENCE 510 AA; 58397 MW; 02DCC7DAED3796E8 CRC64;
 Query Match 100.0%; Score 28; DB 2; Length 510;
 Best Local Similarity 100.0%; Pred. No. 2.4e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
 |||||
 Db 304 GIFFVSYIIISFLVVMNYIAVILENF 331

RESULT 3
 09P2J1 PRELIMINARY; PRT; 519 AA.
 AC 09P2J1;
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE KIAA1356 protein (Fragment).
 GN Name=KIAA1356;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirotsawa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; AB037777; BAA92594.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005151; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005261; P:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR GO; GO:0006814; P:cation ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR Pfam; PF00520; Ion_trans.1.
 DR Pfam; PF0612; IQ.1.
 DR PRINTS; PR00170; NACHANNEL.
 DR SMART; SM00015; IQ; 1.
 DR PROSITE; PSS0096; IQ; 1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 FT NON_TER 1 1
 SQ SEQUENCE 519 AA; 58982 MW; 3E87ED5E26835FC CRC64;

CIN3 RAT
 ID CIN3 RAT STANDARD; PRT; 1951 AA.
 AC P08104;
 DT 01-AUG-1988 (rel. 08, Created)
 DT 01-AUG-1988 (rel. 08, Last sequence update)
 DT 01-OCT-2004 (rel. 45, Last annotation update)
 DE Sodium channel protein type III alpha subunit (Voltage-gated sodium
 DE channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha
 DE subunit) (Voltage-gated sodium channel subtype III).
 GN Name=Scn3a;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Miscar;
 RX MEDLINE=88137594; PubMed=2449363;
 RA Kayano T., Noda M., Flockerzi V., Takahashi H., Numa S.;
 RT "Primary structure of rat brain sodium channel III deduced from the
 RT cDNA sequence.";
 RL FEBS Lett. 228:187-194(1988).
 CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
 CC of excitable membranes. Assuming opened or closed conformations in
 CC response to the voltage difference across the membrane, the
 CC protein forms a sodium-selective channel through which Na(+) ions
 CC may pass in accordance with their electrochemical gradient.
 CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
 CC 3 smaller ones. This sequence represents a large polypeptide.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; Y00766; CA68735.1; -.
 DR PIR; S00320; S00320.
 DR PDB; 1OG9; NMR; A=156-176.
 DR RGD; 3635; Scn3a.
 DR InterPro; IPR001682; Ca/Na_pore.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans.4.
 DR Pfam; PF0612; IQ.1.
 DR Pfam; PF06512; Na_trans_assoc.1.
 DR PRINTS; PR00170; NACHANNEL.
 DR PROSITE; PSS0096; IQ; FALSE NEG.
 KW 3D-structure; Glycoprotein; Ion transport; Ionic channel;
 KW Multigene family; Repeat; Sodium channel; Transmembrane;
 KW Voltage-gated channel.
 FT REPEAT 110 455 I.
 FT REPEAT 693 965 II.
 FT REPEAT 1139 1450 III.
 FT REPEAT 1459 1757 IV.
 FT TRANSMEM 124 147 S1 of repeat I.
 FT TRANSMEM 156 175 S2 of repeat I.
 FT TRANSMEM 189 207 S3 of repeat I.
 FT TRANSMEM 214 233 S4 of repeat I.

RESULT 4

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FT TRANSMEM 249 273 S5 of repeat I.
FT TRANSMEM 401 426 S6 of repeat I.
FT TRANSMEM 706 730 S1 of repeat II.
FT TRANSMEM 742 765 S2 of repeat II.
FT TRANSMEM 774 793 S3 of repeat II.
FT TRANSMEM 800 820 S4 of repeat II.
FT TRANSMEM 836 856 S5 of repeat II.
FT TRANSMEM 910 935 S6 of repeat II.
FT TRANSMEM 1153 1176 S1 of repeat III.
FT TRANSMEM 1190 1215 S2 of repeat III.
FT TRANSMEM 1222 1243 S3 of repeat III.
FT TRANSMEM 1248 1269 S4 of repeat III.
FT TRANSMEM 1289 1310 S5 of repeat III.
FT TRANSMEM 1393 1419 S6 of repeat III.
FT TRANSMEM 1473 1496 S1 of repeat IV.
FT TRANSMEM 1508 1531 S2 of repeat IV.
FT TRANSMEM 1538 1561 S3 of repeat IV.
FT TRANSMEM 1572 1593 S4 of repeat IV.
FT TRANSMEM 1609 1631 S5 of repeat IV.
FT TRANSMEM 1698 1722 S6 of repeat IV.
FT CARBOHYD 211 211 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 290 290 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 296 296 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 302 302 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 307 307 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 339 339 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 424 424 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 835 835 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1002 1002 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1019 1019 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1085 1085 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1317 1317 N-1linked (GlcNAc. . .) (Potential).
FT CARBOHYD 1331 1331 N-1linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 1951 AA; 22135 MW; 74E5E851524BD10E CRC64;

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Query Match 100.0%; Score 28; DB 1; Length 1951;
Best local Similarity 100.0%; Pred. No. 6,5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVLENF 28
Db 1698 GIFFVSYIIISFLVVMNYIAVLENF 1725

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RESULT 5
Q9C007 PRELIMINARY; PRT; 1951 AA.
AC O9C007;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Voltage-gated sodium channel alpha subunit splice variant SCN3A-
DE 8.
GN Name=SCN3A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jeong S.-Y., Goto J., Kanazawa I.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AF225986; AAK00218.1; -.
DR HSSP; P04775; 1BY1.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0005248; P:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006814; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.

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DR InterPro; IPR002111; Cat_channel_TrypL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_Region.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF06512; IQ_1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ_1.
DR PROSITE; PS50096; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1951 AA; 22151 MW; 99AD4C032CE124AB CRC64;

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Query Match 100.0%; Score 28; DB 2; Length 1951;
Best local Similarity 100.0%; Pred. No. 6,5e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVLENF 28
Db 1698 GIFFVSYIIISFLVVMNYIAVLENF 1725

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RESULT 6
Q8IUJ6 PRELIMINARY; PRT; 1961 AA.
AC Q8IUJ6;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Voltage-gated sodium channel alpha 1 subunit.
GN Name=SCN1A;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Uchida M., Ohmori I.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AB098335; BA045228.1; -.
DR HSSP; P04775; 1BY1.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0005248; P:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrypL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_Region.
DR InterPro; IPR005820; M_channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR008051; Na_channel1.
DR InterPro; IPR010526; Na_channel2.
DR InterPro; IPR000100; Ribonuclease_P.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF06512; IQ_1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ_1.
DR PROSITE; PS00648; RIBONUCLEASE_P; UNKNOWN 1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1961 AA; 226201 MW; B1D6946D491B7AD CRC64;

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Query Match 100.0%; Score 28; DB 2; Length 1981;
Best Local Similarity 100.0%; Pred. No. 6.6e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GIFFPVSIIISPLVNNYIAVILNPF 28
DB 1734 GIFFPVSIIISPLVNNYIAVILNPF 1761

RESULT 7
CIN3 HUMAN STANDARD; PRT; 2000 AA.
ID CIN3_HUMAN Q9N46; Q16142; Q9B2B3; Q9C006; Q9MYK2; Q9UPD1; Q9Y6P4;
AC Q9N46; Q16142; Q9B2B3; Q9C006; Q9MYK2; Q9UPD1; Q9Y6P4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Sodium channel protein type III alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.3) (Sodium channel protein, brain III alpha subunit) (Voltage-gated sodium channel subtype III).
DE Name=SCN3A; Synonyms=NAC3;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RA Chen Y., Dale T.J., Romanos M.A., Whitaker W.R., Xie X., Clare J.J.;
RT "Cloning, distribution and functional analysis of the human brain type III sodium channel from human brain."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A. (ISOFORM 3).
RA Jeong S.-Y., Goto J., Kanazawa I.;
RT "Cloning of cDNA for human voltage-gated sodium channel alpha subunit, SCN3A."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A. (ISOFORMS 1: 2; 3 AND 4), AND VARIANT THR-606
RX MEDLINE=21142400; PubMed=112455985; DOI=10.1016/S0378-1119(00)00594-1;
RA Kasei K.-I., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
RA Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT "Genomic structures of SCN2A and SCN3A - candidate genes for deafness at the DFNA16 locus."
RL Gene 264:113-122(2001).
[4]
RN SEQUENCE OF 1-1415 FROM N.A. (ISOFORMS 2 AND 4).
RP TISSUE=Brain;
RC MEDLINE=98251277; PubMed=9589372;
RA Lu C.M., Brown G.B.;
RT "Isolation of a human-brain sodium-channel gene encoding two isoforms of the subtype III alpha-subunit."
RL J. Mol. Neurosci. 10:67-70(1998).
[5]
RN SEQUENCE OF 1324-1413 FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=94211784; PubMed=8159690;
RA Malo M.S., Srivastava K., Andreen J.M., Chen X.N., Korenberg J.R., Ingram V.M.;
RT "Targeted gene walking by low stringency polymerase chain reaction: assignment of a putative human brain sodium channel gene (SCN3A) to RT chromosome 2q24-31."
RL Proc. Natl. Acad. Sci. U.S.A. 91:2975-2979(1994).
[6]
RN SEQUENCE OF 1669-1750 FROM N.A.
RP TISSUE=Kidney;
RC Tomkovich G.S., Kyle J.W.;
RT "Endogenous sodium current in HEK293 cells: increase in cell surface expression of endogenous currents by stable transfection of the Beta 1 subunit."
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in

CC response to the voltage difference across the membrane, the
CC protein forms a sodium-selective channel through which Na(+) ions
CC may pass in accordance with their electrochemical gradient.
CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
CC 3 smaller ones. This sequence represents a large polypeptide.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=Exons 6A and 6N only differ by a single residue;
CC Name=1; Synonyms=6A-12+12b; Sequence=Displayed;
CC IsoId=Q9NY46-1; Sequence=Displayed;
CC Name=2; Synonyms=6A-12;
CC IsoId=Q9NY46-2; Sequence=VSP_001034;
CC Name=3; Synonyms=6N-12+12b;
CC IsoId=Q9NY46-3; Sequence=VSP_001033;
CC Name=4; Synonyms=6N-12;
CC -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
CC segment (S4). Segments S4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; AF251507; CAB85895.1; -;
CC EMBL; AF25987; AAK00219.1; -;
CC EMBL; AF330135; AAG53414.1; -;
CC EMBL; AF330118; AAG53414.1; JOINED.
CC EMBL; AF330129; AAG53414.1; JOINED.
CC EMBL; AF330120; AAG53414.1; JOINED.
CC EMBL; AF330121; AAG53414.1; JOINED.
CC EMBL; AF330122; AAG53414.1; JOINED.
CC EMBL; AF330123; AAG53414.1; JOINED.
CC EMBL; AF330124; AAG53414.1; JOINED.
CC EMBL; AF330125; AAG53414.1; JOINED.
CC EMBL; AF330126; AAG53414.1; JOINED.
CC EMBL; AF330127; AAG53414.1; JOINED.
CC EMBL; AF330128; AAG53414.1; JOINED.
CC EMBL; AF330129; AAG53414.1; JOINED.
CC EMBL; AF330130; AAG53414.1; JOINED.
CC EMBL; AF330131; AAG53414.1; JOINED.
CC EMBL; AF330132; AAG53414.1; JOINED.
CC EMBL; AF330133; AAG53414.1; JOINED.
CC EMBL; AF330134; AAG53414.1; JOINED.
CC EMBL; AF330135; AAG53415.1; -;
CC EMBL; AF330118; AAG53415.1; JOINED.
CC EMBL; AF330119; AAG53415.1; JOINED.
CC EMBL; AF330120; AAG53415.1; JOINED.
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CC EMBL; AF330123; AAG53415.1; JOINED.
CC EMBL; AF330124; AAG53415.1; JOINED.
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CC EMBL; AF330135; AAG53415.1; JOINED.
CC EMBL; AF035685; AAC29514.1; -;
CC EMBL; AF035686; AAC29515.1; -;

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DR EMBL; S69887; AAB30530.1; -.
DR EMBL; AF239921; AAP44690.1; -.
DR PIR; A54937; A54937.
DR HSSP; P04775; 1BXY.
DR Genew; HGNC:10590; SCN3A.
DR MIM; 182391; -.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; NAS.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.
DR GO; GO:0006814; P:sodium ion transport; NAS.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat_channel_TyPL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; Ion_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR010526; Na_channel.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF06512; IQ_1.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS50096; IQ_1.
KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Polymorphism; Repeat; Sodium channel; Transmembrane;
KW Voltage-gated channel.
FT TRANSMEM 124 147
FT TRANSMEM 156 175
FT TRANSMEM 189 207
FT TRANSMEM 214 233
FT TRANSMEM 249 273
FT TRANSMEM 401 426
FT TRANSMEM 451 479
FT TRANSMEM 755 779
FT TRANSMEM 814 842
FT TRANSMEM 893 869
FT TRANSMEM 885 905
FT TRANSMEM 959 984
FT TRANSMEM 1202 1225
FT TRANSMEM 1239 1264
FT TRANSMEM 1271 1292
FT TRANSMEM 1318 1359
FT TRANSMEM 1338 1359
FT TRANSMEM 1442 1468
FT TRANSMEM 1522 1545
FT TRANSMEM 1557 1580
FT TRANSMEM 1587 1610
FT TRANSMEM 1621 1642
FT TRANSMEM 1658 1680
FT TRANSMEM 1747 1771
FT TRANSMEM 1900 1929
FT CARBOHYD 211 211
FT CARBOHYD 290 290
FT CARBOHYD 296 296
FT CARBOHYD 302 302
FT CARBOHYD 307 307
FT CARBOHYD 339 339
FT CARBOHYD 624 624
FT CARBOHYD 884 884
FT CARBOHYD 1051 1051
FT CARBOHYD 1068 1068
FT CARBOHYD 1134 1134
FT CARBOHYD 1366 1366
FT CARBOHYD 1380 1380
FT CARBOHYD 208 208
FT VARSPLIC 625 673
Query Match 100.0%; Score 28; DB 1; Length 2000;
Best Local Similarity 100.0%; Pred. No. 6,7e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
ID CIN2_HUMAN STANDARD; PRT; 2005 AA.
AC Q99250; O14472; Q99250; Q99250;
DT 01-JUN-1994 (Rel. 29, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-FEB-2004 (Rel. 44, Last annotation update)
DE Sodium channel protein type II alpha subunit (Voltage-gated sodium
DE channel alpha subunit Nav1.2) (Sodium channel protein, Brain II alpha
DE subunit) (HSC II).
GN Name=SCN2A; Synonyms=SCN2A2, NAC2;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=92390418; PubMed=1325650;
RA Ahmed C.M., Ware D.H., Lee S.C., Patten C.D., Ferrer-Montiel A.V.,
RA Schinder A.F., McPherson J.D., Wagner-McPherson C.B., Wasmuth J.J.,
RA Evans G.A., Montiel M.;
RT "Primary structure, chromosomal localization, and functional
RT expression of a voltage-gated sodium channel from human brain."
RT Proc. Natl. Acad. Sci. U.S.A. 89:8220-8224(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=21142400; PubMed=11245985; DOI=10.1016/S0378-1119(00)00594-1;
RA Kasai N., Fukushima K., Ueki Y., Prasad S., Nosakowski J.,
RA Sugata K.-I., Sugata A., Nishizaki K., Meyer N.C., Smith R.J.H.;
RT "Genomic structures of SCN2A and SCN3A - candidate genes for deafness
RT at the DFNA16 locus."
RT Gene 264:113-122(2001).
RN [3]
RP SEQUENCE OF 1-89 FROM N.A.
RX Lu C.-M., Eichelberger U.S., Beckman M.L., Schade S.D., Brown G.B.;
RT "Isolation of the 5'-flanking region for human brain sodium channel
RT subtype II alpha-Subunit (SCN2A)."
RT Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 1702-2005 FROM N.A.
RX TISSUE=Brain;
RC MEDLINE=92275082; PubMed=1317301;
RA Lu C.-M., Han U., Rado T.A., Brown G.B.;
RT "Differential expression of two sodium channel subtypes in human
RT brain."
RT FEBS Lett. 303:53-58(1992).
RN [5]
RP SEQUENCE OF 1702-1772 FROM N.A.
RX MEDLINE=91110524; PubMed=1846440;
RA Han U., Lu C.-M., Brown G.B., Rado T.A.;
RT "Direct amplification of a single dissected chromosomal segment by
RT polymerase chain reaction: a human brain sodium channel gene is on
RT chromosome 2q22-q23."
RT Proc. Natl. Acad. Sci. U.S.A. 88:335-339(1991).
RN [6]
RP FUNCTION: Mediates the voltage-dependent sodium ion permeability
RN of excitable membranes. Assuming opened or closed conformations in
RN response to the voltage difference across the membrane, the
RN protein forms a sodium-selective channel through which Na(+) ions
RN may pass in accordance with their electrochemical gradient.
RN 3 smaller ones. This sequence represents a large polypeptide.
RN -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
RN -1- SUBCELLULAR LOCATION: Integral membrane protein.
RN -1- ALTERNATIVE PRODUCTS:
RN Name=1; Synonyms=Adult, 6A;
RN Name=2; Synonyms=Neonatal, 6N;
RN Name=3; Synonyms=Adult, 6A;
RN Name=4; Synonyms=Neonatal, 6N;
RN Name=5; Synonyms=Adult, 6A;
RN Name=6; Synonyms=Neonatal, 6N;
RN Name=7; Synonyms=Adult, 6A;
RN Name=8; Synonyms=Neonatal, 6N;
RN Name=9; Synonyms=Adult, 6A;
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CC segment (s4). Segments s4 are probably the voltage-sensors and are
CC characterized by a series of positively charged amino acids at
CC every third position.
CC -1- SIMILARITY: Belongs to the sodium channel family.
CC -1- SIMILARITY: Contains 1 IQ domain.
CC -----
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DR HSSP, P04775; 1BYV; -;
DR Genew; HGNC:10588; SCN2A2.
DR MIM; 601219; -;
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005248; P:voltage-gated sodium channel activity; TAS.
DR GO; GO:0006814; P:sodium ion transport; TAS.
DR InterPro; IPR001682; Ca/Na_pore; TrpL.
DR InterPro; IPR002111; Cat_channel; TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; Ion_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.

DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF00612; IQ; 1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS50096; IQ; 1.
KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW Multigene family; Repeat; Sodium channel; Transmembrane;
KW Voltage-gated channel.
FT REPEAT 111 456 I.
FT REPEAT 741 1013 II.
FT REPEAT 1190 1504 III.
FT REPEAT 1513 1811 IV.
FT TRANSMEM 125 148 S1 of repeat I.
FT TRANSMEM 157 176 S2 of repeat I.
FT TRANSMEM 190 208 S3 of repeat I.
FT TRANSMEM 215 234 S4 of repeat I.
FT TRANSMEM 251 274 S5 of repeat I.
FT TRANSMEM 402 427 S6 of repeat I.
FT TRANSMEM 754 778 S1 of repeat II.
FT TRANSMEM 790 813 S2 of repeat II.
FT TRANSMEM 822 841 S3 of repeat II.
FT TRANSMEM 848 867 S4 of repeat II.
FT TRANSMEM 884 904 S5 of repeat II.
FT TRANSMEM 958 983 S6 of repeat II.
FT TRANSMEM 1204 1227 S1 of repeat III.
FT TRANSMEM 1241 1266 S2 of repeat III.
FT TRANSMEM 1273 1294 S3 of repeat III.
FT TRANSMEM 1299 1320 S4 of repeat III.
FT TRANSMEM 1340 1367 S5 of repeat III.
FT TRANSMEM 1447 1473 S6 of repeat III.
FT TRANSMEM 1527 1550 S1 of repeat IV.
FT TRANSMEM 1592 1585 S2 of repeat IV.
FT TRANSMEM 1626 1647 S3 of repeat IV.
FT TRANSMEM 1663 1685 S4 of repeat IV.
FT TRANSMEM 1752 1776 S5 of repeat IV.
FT DOMAIN 1905 1934 IQ.
FT CARBOHYD 212 212 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 285 285 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 291 291 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 297 297 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 303 303 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 308 308 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 340 340 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 604 604 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 624 624 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 883 883 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 1055 1055 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 1072 1072 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 1136 1136 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 1368 1368 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 1382 1382 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 1393 1393 N-linked (GlcNAc . .) (Potential).
FT CARBOHYD 1778 1778 N-linked (GlcNAc . .) (Potential).
FT VARSPLIC 209 209 D -> N (in isoform 2).
FT CONFLICT 524 524 /FTId=VSP_001032.
R -> L (in Ref. 1).
Query Match 100.0%; Score 28; DB 1; Length 2005;
Best Local Similarity 100.0%; Pred. No. 6.7e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GIFFVSYIIISPLVNVNYIVIIENF 28
Db 1752 GIFFVSYIIISPLVNVNYIVIIENF 1779
RESULT 9
ID CIN2 RAT STANDARD; PRT; 2005 AA.
AC P04775;
DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Sodium channel protein type II alpha subunit (Voltage-gated sodium
 DE channel alpha subunit Nav1.2) (Sodium channel protein, brain II alpha
 DE subunit).
 GN Name=Scn2a;
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 ON NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86146901; PubMed=3754035;
 RA Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kuraaki M.,
 RA Takahashi H., Numa S.,
 RL "Existence of distinct sodium channel messenger RNAs in rat brain.",
 RL Nature 320:186-192(1986).
 CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability
 CC of excitable membranes. Assuming opened or closed conformations in
 CC response to the voltage difference across the membrane, the
 CC protein forms a sodium-selective channel through which Na(+) ions
 CC may pass in accordance with their electrochemical gradient.
 CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-
 CC 3 smaller ones. This sequence represents a large polypeptide.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
 CC segment (S4). Segments S4 are probably the voltage-sensors and are
 CC characterized by a series of positively charged amino acids at
 CC every third position.
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X03639; CAA27287.1; -
 DR PDB: 1BY7; NMR: A=1474-1526.
 DR InterPro: IPR001682; Ca/Na_pore.
 DR InterPro: IPR002111; Cat_channel_TrypL.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR000048; IQ_region.
 DR InterPro: IPR005820; M-channel_nlg.
 DR InterPro: IPR01656; Na_channel.
 DR Pfam: PF00520; Na_trans_assoc.
 DR Pfam: PF00612; Ion_trans; 4.
 DR Pfam: PF06512; IQ; 1.
 DR PRINTS: PR00170; NACHANNEL.
 DR PROSITE: PS50096; IQ; 1.
 DR 3D-structure; Glycoprotein; Ion transport; Ionic channel;
 DR Multigene family; Repeat; Sodium channel; Transmembrane;
 DR Voltage-gated channel.
 FT REPEAT 111 456 I.
 FT REPEAT 741 1013 II.
 FT REPEAT 1190 1504 III.
 FT REPEAT 1513 1811 IV.
 FT TRANSMEM 125 148 S1 of repeat I.
 FT TRANSMEM 157 176 S2 of repeat I.
 FT TRANSMEM 176 208 S3 of repeat I.
 FT TRANSMEM 215 234 S4 of repeat I.
 FT TRANSMEM 251 274 S5 of repeat I.
 FT TRANSMEM 402 427 S6 of repeat I.
 FT TRANSMEM 754 778 S1 of repeat II.
 FT TRANSMEM 790 813 S2 of repeat II.
 FT TRANSMEM 822 841 S3 of repeat II.
 FT TRANSMEM 848 867 S4 of repeat II.
 FT TRANSMEM 884 904 S5 of repeat II.

FT TRANSMEM 958 983 S6 of repeat II.
 FT TRANSMEM 1204 1227 S1 of repeat III.
 FT TRANSMEM 1241 1266 S2 of repeat III.
 FT TRANSMEM 1273 1294 S3 of repeat III.
 FT TRANSMEM 1299 1320 S4 of repeat III.
 FT TRANSMEM 1340 1367 S5 of repeat III.
 FT TRANSMEM 1447 1473 S6 of repeat III.
 FT TRANSMEM 1527 1550 S1 of repeat IV.
 FT TRANSMEM 1562 1585 S2 of repeat IV.
 FT TRANSMEM 1592 1615 S3 of repeat IV.
 FT TRANSMEM 1626 1647 S4 of repeat IV.
 FT TRANSMEM 1663 1685 S5 of repeat IV.
 FT TRANSMEM 1752 1776 S6 of repeat IV.
 FT DOMAIN 1905 1934 IQ.
 FT CARBOHYD 212 212 N-linked (GlcNAc...)
 FT CARBOHYD 285 285 N-linked (GlcNAc...)
 FT CARBOHYD 291 291 N-linked (GlcNAc...)
 FT CARBOHYD 297 297 N-linked (GlcNAc...)
 FT CARBOHYD 303 303 N-linked (GlcNAc...)
 FT CARBOHYD 308 308 N-linked (GlcNAc...)
 FT CARBOHYD 340 340 N-linked (GlcNAc...)
 FT CARBOHYD 604 604 N-linked (GlcNAc...)
 FT CARBOHYD 624 624 N-linked (GlcNAc...)
 FT CARBOHYD 883 883 N-linked (GlcNAc...)
 FT CARBOHYD 1055 1055 N-linked (GlcNAc...)
 FT CARBOHYD 1072 1072 N-linked (GlcNAc...)
 FT CARBOHYD 1136 1136 N-linked (GlcNAc...)
 FT CARBOHYD 1168 1168 N-linked (GlcNAc...)
 FT CARBOHYD 1382 1382 N-linked (GlcNAc...)
 FT CARBOHYD 1393 1393 N-linked (GlcNAc...)
 SQ SEQUENCE 2005 AA; 227872 MW; 861B583D79F8324 CRC64;
 Query Match 100.0%; Score 28; DB 1; Length 2005;
 Best Local Similarity 100.0%; Pred. No. 6,7e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GIFFPVSYYIIISFLVVMYIAVLENF 28
 Db 1752 GIFFPVSYYIIISFLVVMYIAVLENF 1779
 RESULT 10
 Q9YGN7 PRELIMINARY; PRT; 2007 AA.
 AC Q9YGN7;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Voltage-dependent sodium channel.
 OS Cynops pyrrhogaster (Japanese common newt).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Cynops.
 ON NCBI_TaxID=8330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSTB-Retina;
 RA Hirota K., Kaneko Y., Matsumoto G., Hanyu Y.;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL: AF123593; AAD17315.1; -.
 DR HSR; P04775; 1BY7.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro: IPR001682; Ca/Na_pore.
 DR InterPro: IPR002111; Cat_channel_TrypL.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR005820; M-channel_nlg.

DR InterPro; IPRO01696; Na_channel.
 DR InterPro; IPRO10526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans_4.
 DR Pfam; PF00612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PRO0170; NACHANNEL.
 DR SMART; SM00015; IQ_1.
 KM Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 2007 AA; 228398 MW; 013EB9B9EC9C94C9 CRC64;

Query Match 100.0%; Score 28; DB 2; Length 2007;
 Best Local Similarity 100.0%; Pred. No. 6.7e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFVSYITISFLVVMNYIAVILENF 28
 Db 1754 GIFFVSYITISFLVVMNYIAVILENF 1781

RESULT 11
 CINI_HUMAN STANDARD; PRT; 2009 AA.
 ID CINI_HUMAN
 AC P35498; Q16172; Q96LA3; Q9C008;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sodium channel protein type I alpha subunit (Voltage-gated sodium
 DE channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha
 DE subunit).
 GN Name=SCN1A; Synonym=SCN1, NAC1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RX SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS GEFS+2 MET-875 AND
 RX HIS-1648.
 RX MEDLINE=20206553; PubMed=10742094;
 RA Becay A., MacDonald B.T., Meisler M.H., Baulac S., Huberfeld G.,
 RA An-Goufinkel I., Brice A., LeGuern E., Moulard B., Chaigne D.,
 RA Buresi C., Malafosse A.;
 RT "Mutations of SCN1A, encoding a neuronal sodium channel, in two
 RT families with GEFS+2";
 RL Nat. Genet. 24:343-345(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Jeong S.-Y., Goto J., Kanazawa I.;
 RT "Cloning of cDNA for human voltage-gated sodium channel alpha subunit,
 RT SCN1A";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RA Sugawara T., Mazaki E.M., Yamakawa K.;
 RT "Homo sapiens neuronal voltage-gated sodium channel type I (Nav1.1)
 RT mRNA";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANT THR-1067.
 RA Ouchida M., Ohmori I.;
 RT "Isoforms of human sodium channel SCN1A gene";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1335-1428 FROM N.A.
 RX MEDLINE=94340991; PubMed=8062593;
 RA Malo M.S., Blanchard B.J., Andresen U.M., Srivastava K., Chen X.N.,
 RA Li X., Jabe E.W., Korenberg J.R., Ingram V.M.;
 RT "Localization of a putative human brain sodium channel gene (SCN1A) to
 RT chromosome band 2q24.";
 RL Cytogenet. Cell Genet. 67:178-186(1994).
 RN [6]
 RP SEQUENCE OF 1518-1940 FROM N.A.

RC TISSUE=Brain;
 RX MEDLINE=92275082; PubMed=1317301;
 RA Lu C.-M., Han J., Rado T.A., Brown G.B.;
 RT "Differential expression of two sodium channel subtypes in human
 RT brain";
 RL FEBS Lett. 303:53-58(1992).
 RN [7]
 RP VARIANTS GEFS+2 VAL-188; LEU-1353 AND MET-1656.
 RX MEDLINE=21152274; PubMed=11254444;
 RA Wallace R.H., Scheffer I.E., Barnett S., Richards M., Dibbens L.,
 RA Desai R.R., Lerman-Sagie T., Lev D., Mazali A., Brand N.,
 RA Ben-Zeev B., Golkman I., Singh R., Kremidiotis G., Gardner A.,
 RA Suterland G.R., George A.L. Jr., Mulley J.C., Berkovic S.F.;
 RT "Neuronal sodium-channel alpha1-subunit mutations in generalized
 RT epilepsy with febrile seizures plus";
 RL Am. J. Hum. Genet. 68:859-865(2001).
 RN [8]
 RP VARIANT GEFS+2 ARG-1204.
 RX MEDLINE=21152275; PubMed=11254445;
 RA Becay A., Heils A., MacDonald B.T., Haug K., Sander T., Meisler M.H.;
 RT "A novel SCN1A mutation associated with generalized epilepsy with
 RT febrile seizures plus -- and prevalence of variants in patients with
 RT epilepsy";
 RL Am. J. Hum. Genet. 68:866-873(2001).
 RN [9]
 RP VARIANT SMEI PHE-986.
 RX MEDLINE=21257503; PubMed=11359211;
 RA Claes L., Del-Favero J., Ceulemans B., Lagae L., Van Broeckhoven C.,
 RA De Jonghe P.;
 RT "De novo mutations in the sodium-channel gene SCN1A cause severe
 RT myoclonic epilepsy of infancy";
 RL Am. J. Hum. Genet. 68:1327-1332(2001).
 RN [10]
 RP VARIANT GEFS+2 THR-1270.
 RX MEDLINE=21630138; PubMed=11756608;
 RA Abou-Khalil B., Ge Q., Desai R., Ryther R., Bazyk A., Bailey R.,
 RA Haines J.L., Sutcliffe J.S., George A.L. Jr.;
 RT "Partial and generalized epilepsy with febrile seizures plus and a
 RT novel SCN1A mutation";
 RL Neurology 57:2265-2272(2001).
 RN [11]
 RP FUNCTION: Mediates the voltage-dependent sodium ion permeability
 RP of excitable membranes. Assuming opened or closed conformations in
 RP response to the voltage difference across the membrane, the
 RP protein forms a sodium-selective channel through which Na(+) ions
 RP may pass in accordance with their electrochemical gradient.
 RP SUBUNIT: The sodium channel consists of a large polypeptide and 2-
 RP 3 smaller ones. This sequence represents a large polypeptide.
 RP -1- SUBCELLULAR LOCATION: Integral membrane protein.
 RP -1- ALTERNATIVE PRODUCTS:
 RP Event=Alternative splicing; Named isoforms=2;
 RP Name=1;
 RP IsoId=P35498-1; Sequence=Displayed;
 RP Name=2;
 RP IsoId=P35498-2; Sequence=VSP_001031;
 RP Note=No experimental confirmation available;
 RP -1- DOMAIN: The sequence contains 4 internal repeats, each with 5
 RP hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged
 RP segment (S4). Segments S4 are probably the voltage-sensors and are
 RP characterized by a series of positively charged amino acids at
 RP every third position.
 RP -1- DISEASE: Defects in SCN1A are the cause of generalized epilepsy
 RP with febrile seizures plus type 2 (GEFS+2) [MIM:604233]. This
 RP autosomal dominant disorder is characterized by febrile seizures
 RP in children and afebrile seizures in adults. Penetrance is
 RP incomplete and a large intrafamilial variability of the phenotype
 RP is observed.
 RP -1- DISEASE: Defects in SCN1A are a cause of severe myoclonic epilepsy
 RP in infancy (SMEI) [MIM:607208], a severe form of generalized
 RP epilepsy with febrile seizures. SMEI is a rare disorder
 RP characterized by normal development before onset, seizures
 RP beginning in the first year of life in the form of generalized or
 RP unilateral febrile clonic seizures, secondary appearance of
 RP myoclonic seizures, and occasionally partial seizures. It is

CC associated with ataxia, slowed psychomotor development, and mental decline.

CC -1- SIMILARITY: Belongs to the sodium channel family.

CC -1- SIMILARITY: Contains 1 IQ domain.

CC -----

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CC -----

CC EMBL; AF225985; AAK00217.1; -

CC EMBL; AY043484; AAK95360.1; -

CC EMBL; AB093548; BAC21101.1; -

CC EMBL; AB093549; BAC21102.1; -

CC EMBL; S71446; AAB31605.1; -

CC EMBL; X65362; CAA46439.1; -

CC EMBL; M91803; -; NOT_ANNOTATED_CDS.

CC PIR; I52964; I52964.

CC PIR; S29184; S29184.

CC HSSP; P04775; IBY.

CC Gene; HGNC:10585; SCN1A.

CC MIM; 182389; -

CC MIM; 604233; -

CC MIM; 607208; -

CC GO; GO:0016021; C:integral to membrane; NAS.

CC GO; GO:0005248; F:voltage-gated sodium channel activity; NAS.

CC GO; GO:0006814; P:sodium ion transport; NAS.

CC InterPro; IPR001682; Ca/Na_pore.

CC InterPro; IPR002111; Cat_channel_TpL.

CC InterPro; IPR005821; Ion_trans.

CC InterPro; IPR000048; IQ_region.

CC InterPro; IPR005820; M_channel_nlg.

CC InterPro; IPR008051; Na_channel.

CC InterPro; IPR010526; Na_trans_assoc.

CC Pfam; PF00520; Ion_trans_4.

CC Pfam; PF06512; IQ_1.

CC Pfam; PF06512; Na_trans_assoc; 1.

CC PRINTS; PRO0170; NACHANNEL.

CC PRINTS; PRO1664; NACHANNEL.

CC PROSITE; PS50096; IQ_FALSE_NEG.

CC KW Alternative splicing; Disease mutation; Epilepsy; Glycoprotein; Ion transport; Ionic channel; Multigene family; Polymorphism; Repeat; Sodium channel; Transmembrane; Voltage-gated channel.

CC FT REPEAT 110 454

CC FT REPEAT 750 1022

CC FT REPEAT 1200 1514

CC FT REPEAT 1523 1821

CC FT TRANSMEM 124 147

CC FT TRANSMEM 156 175

CC FT TRANSMEM 189 207

CC FT TRANSMEM 214 223

CC FT TRANSMEM 250 273

CC FT TRANSMEM 400 425

CC FT TRANSMEM 763 787

CC FT TRANSMEM 799 822

CC FT TRANSMEM 831 850

CC FT TRANSMEM 857 876

CC FT TRANSMEM 883 913

CC FT TRANSMEM 967 992

CC FT TRANSMEM 1214 1237

CC FT TRANSMEM 1251 1276

CC FT TRANSMEM 1283 1304

CC FT TRANSMEM 1309 1330

CC FT TRANSMEM 1350 1377

CC FT TRANSMEM 1457 1483

CC FT TRANSMEM 1537 1560

CC FT TRANSMEM 1572 1595

CC FT TRANSMEM 1602 1625

CC TRANSMEM 1636 1657

CC S4 of repeat IV (By similarity).

FT TRANSMEM 1673 1695 S5 of repeat IV (By similarity).

FT TRANSMEM 1762 1786 S6 of repeat IV (By similarity).

FT CARBOHYD 211 211 N-linked (GlcNAc...) (Potential).

Query Match

Best Local Similarity 100.0%; Score 28; DB 1; Length 2009;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFPVSYITISFLVVMNYIAVILLENF 28

DB 1762 GIFFPVSYITISFLVVMNYIAVILLENF 1789

RESULT 12

CIN1 RAT STANDARD; PRT; 2009 AA.

AC P04774;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Sodium channel protein type I alpha subunit (Voltage-gated sodium channel alpha subunit Nav1.1) (Sodium channel protein, brain I alpha subunit).

DE GN Name=Scn1a;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxId=10116;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=86146901; PubMed=3754035;

RA Noda M., Ikeda T., Kayano T., Suzuki H., Takeshima H., Kuraaki M., Takeshahi H., Numa S.;

RT "Existence of distinct sodium channel messenger RNAs in rat brain.";

RL Nature 320:188-192(1986).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=87313395; PubMed=2442385;

RA Noda M., Numa S.;

RT "Structure and function of sodium channel.";

RL J. Recept. Res. 7:467-497(1987).

CC -1- FUNCTION: Mediates the voltage-dependent sodium ion permeability of excitable membranes. Assuming opened or closed conformations in response to the voltage difference across the membrane, the protein forms a sodium-selective channel through which Na(+) ions may pass in accordance with their electrochemical gradient.

CC -1- SUBUNIT: The sodium channel consists of a large polypeptide and 2-3 smaller ones. This sequence represents a large polypeptide.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC DOMAIN: The sequence contains 4 internal repeats, each with 5 hydrophobic segments (S1,S2,S3,S5,S6) and one positively charged segment (S4). Segments S4 are probably the voltage-sensors and are characterized by a series of positively charged amino acids at every third position.

CC -1- SIMILARITY: Belongs to the sodium channel family.

CC -1- SIMILARITY: Contains 1 IQ domain.

CC -----

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CC -----

CC EMBL; X03638; CAA2786.1; -

CC EMBL; M22253; AAK79965.1; -

CC PIR; A25019; A25019.

CC HSSP; P04775; IBY.

CC RGD; 69364; Scn1a.

CC InterPro; IPR001682; Ca/Na_pore.

CC InterPro; IPR002111; Cat_channel_TpL.

CC InterPro; IPR005821; Ion_trans.

DR InterPro; IPR000048; IQ region.
 DR InterPro; IPR005820; M+channel nlg.
 DR InterPro; IPR001696; Na channel.
 DR InterPro; IPR008051; Na channel.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans_4.
 DR Pfam; PF0612; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PRO170; NACHANNEL.
 DR PRINTS; PRO164; NACHANNEL.
 DR PROSITE; PS50096; IQ; FALSE_NEG.
 KW Glycoprotein; Ion transport; Ionic channel; Multigene family; Repeat;
 KW Sodium channel; Transmembrane; Voltage-gated channel.
 FT REPEAT 110 454 I.
 FT REPEAT 750 1022 II.
 FT REPEAT 1200 1514 III.
 FT REPEAT 1523 1821 IV.
 FT TRANSMEM 124 147 S1 of repeat I.
 FT TRANSMEM 156 175 S2 of repeat I.
 FT TRANSMEM 189 207 S3 of repeat I.
 FT TRANSMEM 214 233 S4 of repeat I.
 FT TRANSMEM 250 273 S5 of repeat I.
 FT TRANSMEM 400 425 S6 of repeat I.
 FT TRANSMEM 763 787 S1 of repeat II.
 FT TRANSMEM 799 822 S2 of repeat II.
 FT TRANSMEM 831 850 S3 of repeat II.
 FT TRANSMEM 857 876 S4 of repeat II.
 FT TRANSMEM 893 913 S5 of repeat II.
 FT TRANSMEM 967 992 S6 of repeat II.
 FT TRANSMEM 1214 1237 S1 of repeat III.
 FT TRANSMEM 1251 1276 S2 of repeat III.
 FT TRANSMEM 1283 1304 S3 of repeat III.
 FT TRANSMEM 1309 1330 S4 of repeat III.
 FT TRANSMEM 1350 1377 S5 of repeat III.
 FT TRANSMEM 1457 1483 S6 of repeat III.
 FT TRANSMEM 1537 1560 S1 of repeat IV.
 FT TRANSMEM 1572 1595 S2 of repeat IV.
 FT TRANSMEM 1602 1625 S3 of repeat IV.
 FT TRANSMEM 1636 1657 S4 of repeat IV.
 FT TRANSMEM 1673 1695 S5 of repeat IV.
 FT TRANSMEM 1762 1786 S6 of repeat IV.
 FT CARBOHYD 211 211 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 284 284 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 295 295 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 301 301 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 306 306 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 338 338 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 601 601 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 621 621 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 681 681 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 882 882 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1060 1060 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1064 1064 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1080 1080 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1146 1146 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1378 1378 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1392 1392 N-1-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 1403 1403 N-1-linked (GlcNAc. . .) (Potential).
 FT SEQUENCE 2009 AA; 228769 MW; 6808466F6368373B CRC64;
 Query Match 100.0%; Score 28; DB 1; Length 2009;
 Best Local Similarity 100.0%; Pred. No. 6-7e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched
 DE library, clone:A230052E19 product:sodium channel protein II homolog
 DE (fragment).
 GN Name=A230052E19R1k;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=21085660; PubMed=11217851;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RA The PANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Taahiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubuchi M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Rikazi Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraka T., Hirozane T.,
 RA Horii F., Imetani K., Ishii Y., Itoh M., Kagawa I., Kaubuka T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RA Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK036645; BAC30078.1; -;
 DR MGD; MGI:2444703; A230052E19R1k.

DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO: GO:0005261; F:cation channel activity; IEA.
 DR GO: GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO: GO:0006812; P:cation transport; IEA.
 DR GO: GO:0006814; P:sodium ion transport; IEA.
 DR InterPro: IPR001682; Ca/Na_pore.
 DR InterPro: IPR000048; IQ_region.
 DR Pfam: PF00612; IQ_1.
 DR PRINTS: PR00170; NACHANNEL.
 DR SMART: SM00015; IQ_1.
 DR PROSITE: PS50096; IQ_1.
 KW Ionic channel.
 FT NON_TER 1
 SQ SEQUENCE 253 AA; 29041 MW; B6B1C4CC35A5E571E CRC64;

Query Match 96.4%; Score 27; DB 2; Length 253;
 Best Local Similarity 100.0%; Pred. No. 1,36-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IFPVSYIIISFLVVMNYIAVLENF 28
 Db 1 IFPVSYIIISFLVVMNYIAVLENF 27

RESULT 14
 062205 PRELIMINARY; PRT; 309 AA.
 AC 062205;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Sodium channel 25.
 GN Name=Scn9a;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Jover E., Shah V.;
 RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; L42338; AAA67106.1; -.
 DR MGD; MGI:107636; Scn9a.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0001518; C:voltage-gated sodium channel complex; IEA.
 DR GO: GO:0005261; F:cation channel activity; IEA.
 DR GO: GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO: GO:0006812; P:cation transport; IEA.
 DR GO: GO:0006814; P:sodium ion transport; IEA.
 DR InterPro: IPR001682; Ca/Na_pore.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR000048; IQ_region.
 DR InterPro: IPR005820; M+channel_nlg.
 DR InterPro: IPR001696; Na_channel.
 DR Pfam: PF00520; Ion_trans; 1.
 DR Pfam: PF00612; IQ_1.
 DR PRINTS: PR00170; NACHANNEL.
 DR SMART: SM00015; IQ_1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 309 AA; 34971 MW; 975165758B88D3EC CRC64;

Query Match 85.7%; Score 24; DB 2; Length 309;
 Best Local Similarity 100.0%; Pred. No. 1,4e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 FVSYIIISFLVVMNYIAVLENF 28
 Db 1 FVSYIIISFLVVMNYIAVLENF 27

Db 63 FVSYIIISFLVVMNYIAVLENF 86

RESULT 15
 015858 PRELIMINARY; PRT; 1977 AA.
 AC 015858;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Sodium channel alpha subunit.
 GN Name=hnr-Na;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=thyroid;
 RA MEDLINE=95237189; PubMed=7720699;
 RX Klugbauer N., Lacinova L., Flockezy V., Hofmann P.;
 RT "Structure and functional expression of a new member of the
 RT tetrodotoxin-sensitive voltage-activated sodium channel family from
 RT human neuroendocrine cells."
 RL EMBO J. 14:1084-1090(1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to the sodium channel family.
 DR EMBL; X82835; CAAS8042.1; -.
 DR PIR; S54771; S54771.
 DR HSSP; P04775; 1BYV.
 DR Gene; HGNC:10597; SCN9A.
 DR GO: GO:0005248; F:voltage-gated sodium channel activity; TAS.
 DR GO: GO:0006814; P:sodium ion transport; TAS.
 DR InterPro: IPR001682; Ca/Na_pore.
 DR InterPro: IPR002111; Cat_channel_TpPL.
 DR InterPro: IPR005821; Ion_trans.
 DR InterPro: IPR000048; IQ_region.
 DR InterPro: IPR005820; M+channel_nlg.
 DR InterPro: IPR001696; Na_channel.
 DR InterPro: IPR010526; Na_trans_assoc.
 DR Pfam: PF00520; Ion_trans; 4.
 DR Pfam: PF00612; IQ_1.
 DR Pfam: PF00612; Na_trans_assoc; 1.
 DR PRINTS: PR00170; NACHANNEL.
 DR SMART: SM00015; IQ_1.
 KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KW Transport; Voltage-gated channel.
 SQ SEQUENCE 1977 AA; 225195 MW; 17D67C8C32BC15FB CRC64;

Query Match 85.7%; Score 24; DB 2; Length 1977;
 Best Local Similarity 100.0%; Pred. No. 5,7e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 FVSYIIISFLVVMNYIAVLENF 28
 Db 1729 FVSYIIISFLVVMNYIAVLENF 1752

RESULT 16
 028644 PRELIMINARY; PRT; 1984 AA.
 AC 028644;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Sodium channel alpha-subunit.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand White; TISSUE=Sciatic nerve;

RX MEDLINE=96074641; PubMed=7479931;
 RA Belcher S.M., Zeriallo C.A., Levenson R., Ritchie J.M., Howe J.R.;
 RT "Cloning of a sodium channel alpha subunit from rabbit Schwann
 cells."
 RL Proc. Natl. Acad. Sci. U.S.A. 92:11034-11038(1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; U55238; AAB89159.1; -.
 DR HSSP; P04775; 1BYV.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001515; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na.pore.
 DR InterPro; IPR002111; Cat_channel_TrypL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel_nlg.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans; 4.
 DR Pfam; PF06512; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR SMART; SM00015; IQ_1.
 DR Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KM Transport; Voltage-gated channel.
 SQ SEQUENCE 1984 AA; 225748 MW; 98F76860C9866AA0 CRC64;

Query Match 85.7%; Score 24; DB 2; Length 1984;
 Best Local Similarity 100.0%; Pred. No. 5.8e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVSYIIISFLVVMNYIAVILENF 28
 Db 1737 FVSYIIISFLVVMNYIAVILENF 1760

RESULT 17
 ID 008562 PRELIMINARY; PRT; 1984 AA.
 AC 008562;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE PNI (Voltage-gated sodium channel) (Fragment).
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97188502; PubMed=9037087;
 RA Toledo-Arai J.J., Mose B.L., He Z.J., Kozowski A.G., Whisenand T.,
 Levinson S.R., Wolf J.J., Silos-Santiago I., Halesova S., Mandel G.;
 RT "Identification of PNI, a predominant voltage-dependent sodium channel
 expressed principally in peripheral neurons."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:1527-1532(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97007982; PubMed=8654872;
 RA Kozak C.A., Sangameswaran L.;
 RT "Genetic mapping of the peripheral sodium channel genes, Scn5a and
 Scn10a, in the mouse."
 RL Mamm. Genome 7:787-788(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Sangameswaran L., Fish L.M., Koch B.D., Rabert D.K., Delgado S.G.,
 Rlinck M., Jakeman L.B., Novakovic S., Wong K., Sze P., Tzoumaka E.,
 Stewart G.R., Herman R.C., Chan H., Eglen R.M., Hunter J.C.;
 RT "A novel tetrodotoxin-sensitive, voltage-gated sodium channel

RT expressed in rat and human dorsal root ganglia.";
 RL J. Biol. Chem. 0:0-0(1997).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL; U7568; AAB50403.1; -.
 DR EMBL; AF000368; AAB80701.1; -.
 DR HSSP; P04775; 1BYV.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0001515; C:voltage-gated sodium channel complex; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:sodium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na.pore.
 DR InterPro; IPR002111; Cat_channel_TrypL.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR005820; M+channel_nlg.
 DR InterPro; IPR001696; Na_channel.
 DR InterPro; IPR010526; Na_trans_assoc.
 DR Pfam; PF00520; Ion_trans; 4.
 DR Pfam; PF06512; IQ_1.
 DR Pfam; PF06512; Na_trans_assoc; 1.
 DR PRINTS; PR00170; NACHANNEL.
 DR SMART; SM00015; IQ_1.
 DR Ion transport; Ionic channel; Sodium channel; Transmembrane;
 KM Transport; Voltage-gated channel.
 FT NON_TER
 SQ SEQUENCE 1984 AA; 226037 MW; 386C389B5097091 CRC64;

Query Match 85.7%; Score 24; DB 2; Length 1984;
 Best Local Similarity 100.0%; Pred. No. 5.8e-15;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVSYIIISFLVVMNYIAVILENF 28
 Db 1738 FVSYIIISFLVVMNYIAVILENF 1761

RESULT 18
 ID 054811 PRELIMINARY; PRT; 279 AA.
 AC 054811;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE GPBI (Fragment).
 OS Cavia porcellus (Guinea pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RX MEDLINE=97338144; PubMed=9192691;
 RA de Miera E.V.S., Rudy B., Sugimori M., Llinas R.;
 RT "Molecular characterization of the sodium channel subunits expressed
 in mammalian cerebellar Purkinje cells."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:7059-7064(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RA Vega-Saenz de Miera E., Rudy B., Sugimori M., Llinas R.;
 RT Submitted (May-1997) to the EMBL/GenBank/DBD databases.
 DR EMBL; AF003372; AAC02899.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
 DR GO; GO:0005261; F:cation channel activity; IEA.
 DR GO; GO:0005248; F:voltage-gated potassium channel activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006814; P:potassium ion transport; IEA.
 DR InterPro; IPR001682; Ca/Na.pore.
 DR InterPro; IPR005821; Ion_trans.


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DR InterPro; IPR003091; K_channel.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR00169; KCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
PT NON_TER 279 279
SQ SEQUENCE 279 AA; 31625 MW; 1504A333CA63DD24 CRC64;

Query Match 60.7%; Score 17; DB 2; Length 279;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFPVSYIIISFLVV 17
DB 263 GIFFPVSYIIISFLVV 279

RESULT 19
P0670 PRELIMINARY; PRT; 1993 AA.
AC P0670;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sodium channel alpha-subunit SCAP1.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidae;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nervous system;
MEDLINE=97238630; PubMed=9115644;
RA Dyer J.R., Johnston W.L., Castellucci V.F., Dunn R.J.;
RT "Cloning and tissue distribution of the Aplysia Na+ channel alpha-
RT subunit cDNA." 16347-356(1997).
RL DNA Cell Biol. 16:347-356(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; U66915; AAC47457.1; -.
DR PIR; T30902; T30902.
DR HSSP; P04775; 1BY.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005248; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1993 AA; 22586 MW; 33E174B9BF07E1A7 CRC64;

Query Match 60.7%; Score 17; DB 2; Length 1993;
Best Local Similarity 100.0%; Pred. No. 4.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SFLVVNMVYAVILENF 28
DB 1719 SFLVVNMVYAVILENF 1735

RESULT 20
Q9IBF1

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ID Q9IBF1 PRELIMINARY; PRT; 1880 AA.
AC Q9IBF1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Voltage-gated sodium channel.
DE Takifugu pardalis (Puffer puffer).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphi; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=98921;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
MEDLINE=20090650; PubMed=10623632;
RA Yotsu-Yamashita M., Nishimori K., Nitanai Y., Isemura M., Sugimoto A.,
RA Yasumoto T.;
RT "Binding properties of 3H-PbTx-3 and 3H-saxitoxin to brain membranes
RT and to skeletal muscle membranes of puffer fish Takifugu pardalis, and the
RT primary structure of a voltage-gated Na+ channel alpha-subunit (fMna1)
RT from skeletal muscle of F. pardalis." 267:403-412(2000).
RL Biochem. Biophys. Res. Commun. 267:403-412(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AB030482; BAA90398.1; -.
DR HSSP; P04775; 1BY.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005248; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M+channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans_4.
DR Pfam; PF00612; IQ_1.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR PROSITE; PS50096; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
SQ SEQUENCE 1880 AA; 21208 MW; 406483C6C3D43E02 CRC64;

Query Match 57.1%; Score 16; DB 2; Length 1880;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SYIIISFLVVNMVYIA 22
DB 1608 SYIIISFLVVNMVYIA 1623

RESULT 21
OS4812 PRELIMINARY; PRT; 278 AA.
ID OS4812;
AC OS4812;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ceriiti (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;

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RX MEDLINE=97338144; PubMed=9192691;
RA de Miera E.V.S., Rudy B., Sugimori M., Llinas R.;
RT "Molecular characterization of the sodium channel subunits expressed
RT in mammalian cerebellar Purkinje cells";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7059-7064(1997).
RN (12)
RN SEQUENCE FROM N.A.
RP TISSUE=Cerebellum;
RA Vega-Saenz de Miera E., Rudy B., Sugimori M., Llinas R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003373; AAC02900.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore..
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR003091; K_channel.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR00169; KCHANNEL.
DR ION_TRANSPORT; Ionic channel; Transmembrane; Transport.
DR NON_TER 278
DR SEQUENCE 278 AA; 31866 MW; 65741B14C6A649A CRC64;

Query Match 50.0%; Score 14; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 9.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFFVSYYIIISFL 14
DB 262 GIFFFVSYYIIISFL 275

RESULT 22
063360 PRELIMINARY; PRT; 324 AA.
AC 063360;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Na+ channel (Fragment).
CN Name=Na+ channel; (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN (1)
RN SEQUENCE FROM N.A.
RP TISSUE=Myocardium;
RA MEDLINE=89292178; PubMed=2544627;
RA Sills M.N., Xu Y.C., Baracchini E., Goodman R.H., Cooperman S.S.,
RA Mandel G., Chien K.R.;
RT "Expression of diverse Na+ channel messenger RNAs in rat myocardium:
RT Evidence for a cardiac-specific Na+ channel.";
RL J. Clin. Invest. 84:331-336(1989).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; M27223; AAA1666.1; -.
DR PIR; A45752; A45752.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0005249; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TpPL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF00612; IQ; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS50096; IQ; 1.
DR ION_TRANSPORT; Ionic channel; Sodium channel; Transmembrane;
DR Transport; Voltage-gated channel.
FT NON_TER 364
FT SEQUENCE 364 AA; 41263 MW; BA5760C962BB6786 CRC64;

Query Match 50.0%; Score 14; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFFVSYYIIISFL 14
DB 131 GIFFFVSYYIIISFL 144

RESULT 24

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DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF00612; IQ; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS50096; IQ; 1.
DR ION_TRANSPORT; Ionic channel; Sodium channel; Transmembrane;
DR Transport; Voltage-gated channel.
FT NON_TER 1
FT SEQUENCE 324 AA; 36863 MW; 95CBE148B354E198 CRC64;

Query Match 50.0%; Score 14; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFFVSYYIIISFL 14
DB 86 GIFFFVSYYIIISFL 99

RESULT 23
09206 PRELIMINARY; PRT; 364 AA.
ID 09206
AC 09206;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Voltage-gated sodium channel alpha subunit (Fragment).
GN Homo sapiens (Human).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RN SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RA Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AB037525; BAA90445.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005261; P:cation channel activity; IEA.
DR GO; GO:0005249; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TpPL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF00612; IQ; 1.
DR PRINTS; PR00170; NACHANNEL.
DR SMART; SM00015; IQ; 1.
DR PROSITE; PS50096; IQ; 1.
DR ION_TRANSPORT; Ionic channel; Sodium channel; Transmembrane;
DR Transport; Voltage-gated channel.
FT NON_TER 364
FT SEQUENCE 364 AA; 41263 MW; BA5760C962BB6786 CRC64;

Query Match 50.0%; Score 14; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFFVSYYIIISFL 14
DB 131 GIFFFVSYYIIISFL 144

RESULT 24

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Q9N2E3
ID Q9N2E3 PRELIMINARY; PRT; 364 AA.
AC Q9N2E3;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Voltage-gated sodium channel alpha subunit (Fragment).
GN Name=SCN8A;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AB037528; BAA90448.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005248; F:cation channel activity; IEA.
DR GO; GO:0006812; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M-channel_nlg.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR00612; IQ_1.
DR SMART; SM00015; IQ_1.
DR PROSITE; PS50096; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KM Transport; Voltage-gated channel.
FT NON_TER 1
FT NON_TER 364
SQ SEQUENCE 364 AA; 41235 MW; 975760C962BE6791 CRC64;

Query Match 50.0%; Score 14; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFVSYIIISPL 14
Db 131 GIFFVSYIIISPL 144

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RESULT 25
Q9N2E4
ID Q9N2E4 PRELIMINARY; PRT; 364 AA.
AC Q9N2E4;
DT 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Voltage-gated sodium channel alpha subunit (Fragment).
GN Name=SCN8A;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; AB037527; BAA90447.1; -.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0006812; F:cation channel activity; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.

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DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na_pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR000048; IQ_region.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR00612; IQ_1.
DR PROSITE; PS50096; IQ_1.
KW Ion transport; Ionic channel; Sodium channel; Transmembrane;
KM Transport; Voltage-gated channel.
FT NON_TER 1
FT NON_TER 364
SQ SEQUENCE 364 AA; 41263 MW; BA5760C962BE6786 CRC64;

Query Match 50.0%; Score 14; DB 2; Length 364;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFVSYIIISPL 14
Db 131 GIFFVSYIIISPL 144

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Search completed: January 27, 2005, 17:51:35
Job time : 94.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 27, 2005, 17:36:50 ; Search time 22.5 Seconds
(without alignments)
82.529 Million cell updates/sec

Title: US-10-608-584-29
Perfect score: 28
Sequence: 1 GIFFFVXYIISFLVVMYIAVLBNF 28

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6C_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	28	100.0	310	3	US-08-605-284B-13
2	28	100.0	310	3	US-08-605-284B-14
3	28	100.0	310	3	US-08-605-284B-15
4	28	100.0	2005	3	US-08-836-325-7
5	28	100.0	2005	4	US-09-457-571-7
6	27	96.4	309	3	US-08-605-284B-4
7	27	96.4	309	3	US-08-605-284B-5
8	25	89.3	813	3	US-08-836-325-8
9	25	89.3	813	4	US-09-457-571-8
10	24	85.7	1011	3	US-08-836-325-2
11	24	85.7	1011	4	US-09-457-571-2
12	24	85.7	1835	3	US-08-836-325-15
13	24	85.7	1835	4	US-09-457-571-15
14	24	85.7	1969	4	US-08-836-325-16
15	24	85.7	1969	4	US-09-457-571-16
16	24	85.7	1977	4	US-09-976-594-757
17	24	85.7	1977	4	US-09-919-039-367
18	24	85.7	1984	3	US-08-836-325-10
19	24	85.7	1984	4	US-09-457-571-10
20	24	85.7	1989	3	US-08-836-325-11
21	24	85.7	1989	3	US-08-836-325-12
22	24	85.7	1989	4	US-09-457-571-11
23	24	85.7	1989	4	US-09-457-571-12
24	17	60.7	310	3	US-08-605-284B-16
25	16	57.1	310	3	US-08-605-284B-10
26	14	50.0	232	3	US-09-024-020B-6
27	14	50.0	232	3	US-09-425-043-6

28	14	50.0	309	3	US-08-605-284B-6	Sequence 6, Appli
29	14	50.0	1976	3	US-09-024-020B-9	Sequence 9, Appli
30	14	50.0	1976	3	US-09-425-043-9	Sequence 9, Appli
31	14	50.0	1978	3	US-09-024-020B-3	Sequence 3, Appli
32	14	50.0	1978	3	US-09-425-043-3	Sequence 3, Appli
33	14	50.0	1988	3	US-09-024-020B-4	Sequence 4, Appli
34	14	50.0	1988	3	US-09-425-043-4	Sequence 4, Appli
35	13	46.4	311	3	US-08-605-284B-23	Sequence 23, Appli
36	13	46.4	521	4	US-08-669-656A-4	Sequence 2, Appli
37	13	46.4	1765	4	US-09-354-147C-2	Sequence 2, Appli
38	13	46.4	1765	4	US-09-354-147C-3	Sequence 3, Appli
39	13	46.4	1765	4	US-09-354-147C-5	Sequence 5, Appli
40	13	46.4	1791	4	US-09-354-147C-42	Sequence 42, Appli
41	13	46.4	1956	3	US-08-843-417-2	Sequence 2, Appli
42	13	46.4	1956	3	US-08-843-417-10	Sequence 10, Appli
43	13	46.4	1956	4	US-09-527-013-2	Sequence 2, Appli
44	13	46.4	1956	4	US-09-527-013-10	Sequence 10, Appli
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46	13	46.4	1957	4	US-08-669-656A-8	Sequence 8, Appli
47	13	46.4	2132	4	US-08-669-656A-6	Sequence 6, Appli
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49	11	39.3	312	3	US-08-605-284B-17	Sequence 17, Appli
50	11	39.3	317	3	US-08-605-284B-19	Sequence 19, Appli
51	10	35.7	307	3	US-08-605-284B-19	Sequence 19, Appli
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53	10	35.7	452	3	US-07-998-289B-6	Sequence 6, Appli
54	10	35.7	1820	3	US-07-998-289B-8	Sequence 8, Appli
55	10	35.7	2100	2	US-08-808-793-23	Sequence 23, Appli
56	10	35.7	2100	2	US-08-772-512A-19	Sequence 19, Appli
57	10	35.7	2104	2	US-08-808-793-4	Sequence 4, Appli
58	10	35.7	2104	2	US-08-772-512A-4	Sequence 4, Appli
59	10	35.7	2105	2	US-08-808-793-3	Sequence 3, Appli
60	10	35.7	2105	3	US-08-772-512A-3	Sequence 3, Appli
61	8	28.6	1836	3	US-08-605-284B-12	Sequence 12, Appli
62	8	28.6	1836	4	US-10-162-012-24	Sequence 24, Appli
63	7	25.0	24	2	US-08-295-643-4	Sequence 4, Appli
64	7	25.0	24	2	US-08-473-265-3	Sequence 3, Appli
65	7	25.0	309	3	US-08-284-747-3	Sequence 3, Appli
66	7	25.0	309	3	US-08-605-284B-11	Sequence 11, Appli
67	7	25.0	2016	3	US-09-634-920-4	Sequence 4, Appli
68	7	25.0	2016	4	US-09-514-907A-2	Sequence 2, Appli
69	7	25.0	2016	4	US-09-896-994-2	Sequence 2, Appli
70	7	25.0	2016	4	US-09-840-125-4	Sequence 4, Appli
71	6	21.4	64	4	US-09-248-796A-23205	Sequence 23205, A
72	6	21.4	77	4	US-09-513-999C-7113	Sequence 7113, Ap
73	6	21.4	84	4	US-09-270-767-22717	Sequence 72717, A
74	6	21.4	84	4	US-09-270-767-47934	Sequence 47934, A
75	6	21.4	103	4	US-09-710-279-1708	Sequence 1708, Ap
76	6	21.4	103	4	US-09-710-279-2074	Sequence 2074, Ap
77	6	21.4	110	4	US-09-248-796A-21277	Sequence 21277, A
78	6	21.4	120	4	US-09-253-991A-26987	Sequence 26987, A
79	6	21.4	127	4	US-09-583-110-4717	Sequence 4717, Ap
80	6	21.4	167	4	US-09-270-767-37083	Sequence 37083, A
81	6	21.4	167	4	US-09-270-767-52300	Sequence 52300, A
82	6	21.4	170	3	US-09-393-245-4	Sequence 4, Appli
83	6	21.4	171	4	US-09-134-000C-5689	Sequence 5689, Ap
84	6	21.4	176	4	US-09-248-796A-18882	Sequence 18882, A
85	6	21.4	195	4	US-09-107-532A-3888	Sequence 3888, Ap
86	6	21.4	195	3	US-09-134-001C-4286	Sequence 4286, Ap
87	6	21.4	204	4	US-09-270-767-56679	Sequence 56679, A
88	6	21.4	210	4	US-09-270-767-39769	Sequence 39769, A
89	6	21.4	230	4	US-09-270-767-54986	Sequence 54986, A
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92	6	21.4	246	4	US-09-583-110-4242	Sequence 4242, Ap
93	6	21.4	273	4	US-09-396-149-12	Sequence 12, Appli
94	6	21.4	273	4	US-09-396-149-14	Sequence 14, Appli
95	6	21.4	273	4	US-09-396-149-16	Sequence 16, Appli
96	6	21.4	273	4	US-09-396-149-20	Sequence 20, Appli
97	6	21.4	273	4	US-09-396-149-22	Sequence 22, Appli
98	6	21.4	300	4	US-09-393-634-42	Sequence 62, Appli
99	6	21.4	316	4	US-09-583-110-4475	Sequence 4475, Ap
100	6	21.4	318	4	US-09-396-149-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1

US-08-605-284B-13
Sequence 13, Application US/08605284B
Patent No. 6060271
GENERAL INFORMATION:
APPLICANT: WALEWSKI, JOSE L.
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1636
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-284B-13

Query Match

Best Local Similarity 100.0%; Score 28; DB 3; Length 310;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFFVSYIIISFLVVMNYIAVILENF 28

Db 283 GIFFFVSYIIISFLVVMNYIAVILENF 310

RESULT 2

US-08-605-284B-14
Sequence 14, Application US/08605284B
Patent No. 6060271
GENERAL INFORMATION:
APPLICANT: WALEWSKI, JOSE L.
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1636
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-284B-14

Query Match

Best Local Similarity 100.0%; Score 28; DB 3; Length 310;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFFVSYIIISFLVVMNYIAVILENF 28

Db 283 GIFFFVSYIIISFLVVMNYIAVILENF 310

RESULT 3

US-08-605-284B-15
Sequence 15, Application US/08605284B
Patent No. 6060271
GENERAL INFORMATION:
APPLICANT: WALEWSKI, JOSE L.
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
TITLE OF INVENTION: HUMAN PERIPHERAL NERVE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1636
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-605-284B-15

Query Match 100.0%; Score 28; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 5.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
|||
Db 283 GIFFVSYIIISFLVVMNYIAVILENF 310

RESULT 4

US-08-836-325-7
; Sequence 7, Application US/08836325
; Patent No. 6110672

GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-836-325-7

Query Match 100.0%; Score 28; DB 3; Length 2005;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
|||
Db 1 GIFFVSYIIISFLVVMNYIAVILENF 28

Db 1752 GIFFVSYIIISFLVVMNYIAVILENF 1779

RESULT 5

US-09-457-571-7
; Sequence 7, Application US/09457571
; Patent No. 6703486

GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-457-571-7

Query Match 100.0%; Score 28; DB 4; Length 2005;
Best Local Similarity 100.0%; Pred. No. 2.9e-20;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
|||
Db 1752 GIFFVSYIIISFLVVMNYIAVILENF 1779

RESULT 6
US-08-605-284B-4
; Sequence 4, Application US/08605284B
; Patent No. 6060271

Qy 1 GIFFVSYIIISFLVVMNYIAVILENF 28
|||
Db 1 GIFFVSYIIISFLVVMNYIAVILENF 28

```

GENERAL INFORMATION:
APPLICANT: WALEMSKI, JOSE L.
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON, HARGRAVE, DEVANS & DOYLE LLP
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-284B-4

Query Match
Best Local Similarity 96.4%; Score 27; DB 3; Length 309;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GIFFFVSIIISFLVVMNYAVILEN 27
283 GIFFFVSIIISFLVVMNYAVILEN 309

```

```

GENERAL INFORMATION:
APPLICANT: WALEMSKI, JOSE L.
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: NIXON, HARGRAVE, DEVANS & DOYLE LLP
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-284B-5

Query Match
Best Local Similarity 96.4%; Score 27; DB 3; Length 309;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GIFFFVSIIISFLVVMNYAVILEN 27
283 GIFFFVSIIISFLVVMNYAVILEN 309

RESULT 8
US-08-836-325-8
Sequence 8, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halsegou, Simon
TITLE OF INVENTION: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational,
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

```

LENGTH: 813 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-325-8

Query Match 89.3%; Score 25; DB 3; Length 813;
Best Local Similarity 100.0%; Pred. No. 1.4e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FVSYYIIISFLVVMNYIAVLENF 28
|||||
Db 617 FVSYYIIISFLVVMNYIAVLENF 641

RESULT 9
US-09-457-571-8
Sequence 8, Application US/09457571
Patent No. 6703486

GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-457-571-8

Query Match 89.3%; Score 25; DB 4; Length 813;
Best Local Similarity 100.0%; Pred. No. 1.4e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 FVSYYIIISFLVVMNYIAVLENF 28
|||||
Db 617 FVSYYIIISFLVVMNYIAVLENF 641

RESULT 10
US-08-836-325-2
Sequence 2, Application US/08836325
Patent No. 6110672

GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1011 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-2

Query Match 85.7%; Score 24; DB 3; Length 1011;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVSYYIIISFLVVMNYIAVLENF 28
|||||
Db 785 FVSYYIIISFLVVMNYIAVLENF 808

RESULT 11

US-09-457-571-2
; Sequence 2, Application US/09457571
; Patent No. 6703486
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/457,571
; FILING DATE: 09-DEC-1999
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/836,325
; FILING DATE: 02-MAY-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1011 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-457-571-2

Query Match 85.7%; Score 24; DB 4; Length 1011;
Best Local Similarity 100.0%; Pred. No. 18e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FVSYIIISFLVVMNYIAVILENF 28
Db 785 FVSYIIISFLVVMNYIAVILENF 808

RESULT 12
US-08-836-325-15
; Sequence 15, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific

; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1835 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; US-08-836-325-15

Query Match 85.7%; Score 24; DB 3; Length 1835;
Best Local Similarity 100.0%; Pred. No. 3.1e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FVSYIIISFLVVMNYIAVILENF 28
Db 1604 FVSYIIISFLVVMNYIAVILENF 1627

RESULT 13
US-09-457-571-15
; Sequence 15, Application US/09457571
; Patent No. 6703486
; GENERAL INFORMATION:
; APPLICANT: Mandel, Gail
; APPLICANT: Halegoua, Simon
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC

COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/457,571
 FILING DATE: 09-DEC-1999
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/836,325
 FILING DATE: 02-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/14251
 FILING DATE: 02-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/482,401
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/334,029
 FILING DATE: 02-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.
 REGISTRATION NUMBER: 36,203
 REFERENCE/DOCKET NUMBER: 0917.0240003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1835 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 US-09-457-571-15

Query Match 85.7%; Score 24; DB 4; Length 1835;
 Best Local Similarity 100.0%; Pred. No. 3.1e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FVSYSIIISFLVVMNYIAVILENF 28
 DB 1604 FVSYSIIISFLVVMNYIAVILENF 1627
 RESULT 14
 US-08-836-325-16
 Sequence 16, Application US/08836325
 Patent No. 6110672
 GENERAL INFORMATION:
 APPLICANT: Mandel, Gail
 APPLICANT: Halegoua, Simon
 TITLE OF INVENTION: Peripheral Nervous System Specific
 TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
 TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
 TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
 STREET: 1100 New York Ave., N. W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/836,325
 FILING DATE: 2-MAY-1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/14251
 FILING DATE: 02-NOV-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/482,401
 FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/334,029
 FILING DATE: 02-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Ludwig, Steven R.
 REGISTRATION NUMBER: 36,203
 REFERENCE/DOCKET NUMBER: 0917.0240002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1969 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-836-325-16

Query Match 85.7%; Score 24; DB 3; Length 1969;
 Best Local Similarity 100.0%; Pred. No. 3.3e-16;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 FVSYSIIISFLVVMNYIAVILENF 28
 DB 1721 FVSYSIIISFLVVMNYIAVILENF 1744
 RESULT 15
 US-09-457-571-16
 Sequence 16, Application US/09457571
 Patent No. 6703486
 GENERAL INFORMATION:
 APPLICANT: Mandel, Gail
 APPLICANT: Halegoua, Simon
 TITLE OF INVENTION: Peripheral Nervous System Specific
 TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
 TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
 TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
 TITLE OF INVENTION: Thereof
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
 STREET: 1100 New York Ave., N. W., Suite 600
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/457,571
 FILING DATE: 09-DEC-1999
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/836,325
 FILING DATE: 02-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/14251

;; FILING DATE: 02-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/482,401
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/334,029
;; FILING DATE: 02-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ludwig, Steven R.
;; REGISTRATION NUMBER: 36,203
;; REFERENCE/DOCKET NUMBER: 0917.0240003
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 16:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1969 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-457-571-16

Query Match 85.7%; Score 24; DB 4; Length 1969;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FVSYYIIISFLVVMNYIAVILENF 28
Db 1721 FVSYYIIISFLVVMNYIAVILENF 1744

RESULT 16
US-09-976-594-757
; Sequence 757, Application US/0976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 757
; LENGTH: 1977
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1719478CD1
US-09-976-594-757

Query Match 85.7%; Score 24; DB 4; Length 1977;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FVSYYIIISFLVVMNYIAVILENF 28
Db 1729 FVSYYIIISFLVVMNYIAVILENF 1752

RESULT 17
US-09-919-039-367
; Sequence 367, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaseer, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US

;; CURRENT APPLICATION NUMBER: US/09/919,039
;; CURRENT FILING DATE: 2002-09-09
;; PRIOR APPLICATION NUMBER: 60/222,113
;; PRIOR FILING DATE: 2000-07-28
;; NUMBER OF SEQ ID NOS: 401
;; SOFTWARE: PERL Program
;; SEQ ID NO 367
;; LENGTH: 1977
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc feature
;; OTHER INFORMATION: Incyte ID No. 6727066 1719478CD1
US-09-919-039-367

Query Match 85.7%; Score 24; DB 4; Length 1977;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FVSYYIIISFLVVMNYIAVILENF 28
Db 1729 FVSYYIIISFLVVMNYIAVILENF 1752

RESULT 18
US-08-836-325-10
; Sequence 10, Application US/08836325
; Patent No. 6110672
; GENERAL INFORMATION:
; APPLICANT: Mandel, Galil
; APPLICANT: Halegoua, Simon
; APPLICANT: Borden, Laurence A.
; TITLE OF INVENTION: Peripheral Nervous System Specific
; TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
; TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
; TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
; THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C
; STREET: 1100 New York Ave., N. W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,325
; FILING DATE: 2-MAY-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/14251
; FILING DATE: 02-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/482,401
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/334,029
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0917.0240002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1984 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-836-325-10

Query Match 85.7%; Score 24; DB 3; Length 1984;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FVSYYIISFLVVMYIAVLENF 28
DB 1738 FVSYYIISFLVVMYIAVLENF 1761

RESULT 19
US-09-457-571-10
Sequence 10, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halogoua, Simon
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1984 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-457-571-10

Query Match 85.7%; Score 24; DB 4; Length 1984;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVSYYIISFLVVMYIAVLENF 28
DB 1738 FVSYYIISFLVVMYIAVLENF 1761

RESULT 20
US-08-836-325-11
Sequence 11, Application US/08836325
Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halogoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C
STREET: 1100 New York Ave., N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-836-325-11

Query Match 85.7%; Score 24; DB 3; Length 1989;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 FVSYYIISFLVVMYIAVLENF 28
DB 1740 FVSYYIISFLVVMYIAVLENF 1763

RESULT 21
US-08-836-325-12
Sequence 12, Application US/08836325

Patent No. 6110672
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,325
FILING DATE: 2-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-836-325-12

Query Match 85.7%; Score 24; DB 3; Length 1989;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVSYYIIISFLVVVMYIAVILENF 28
DB 1740 FVSYYIIISFLVVVMYIAVILENF 1763

RESULT 22
US-09-457-571-11
Sequence 11, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
Thereof

NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917.0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-457-571-11

Query Match 85.7%; Score 24; DB 4; Length 1989;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVSYYIIISFLVVVMYIAVILENF 28
DB 1740 FVSYYIIISFLVVVMYIAVILENF 1763

RESULT 23
US-09-457-571-12
Sequence 12, Application US/09457571
Patent No. 6703486
GENERAL INFORMATION:
APPLICANT: Mandel, Gail
APPLICANT: Halegoua, Simon
APPLICANT: Borden, Laurence A.
TITLE OF INVENTION: Peripheral Nervous System Specific
TITLE OF INVENTION: Sodium Channels, DNA Encoding Therefor, Crystallization,
TITLE OF INVENTION: X-ray Diffraction, Computer Molecular Modeling, Rational
TITLE OF INVENTION: Drug Design, Drug Screening, and Methods of Making and Using
Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Ave., N. W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA

ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/457,571
FILING DATE: 09-DEC-1999
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836,325
FILING DATE: 02-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/14251
FILING DATE: 02-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/482,401
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/334,029
FILING DATE: 02-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0917,0240003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1989 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-457-571-12

Query Match 85.7%; Score 24; DB 4; Length 1989;
Best Local Similarity 100.0%; Pred. No. 3.3e-16;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FVSIIISFLVVMYIAVLENF 28
DB 1740 FVSIIISFLVVMYIAVLENF 1763

RESULT 24
US-08-605-284B-16
Sequence 16, Application US/08605284B
Patent No. 6060271
GENERAL INFORMATION:
APPLICANT: MALEWSKI, JOSE L.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-284B-16

Query Match 60.7%; Score 17; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 7.9e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SFLVVMYIAVLENF 28
DB 294 SFLVVMYIAVLENF 310

RESULT 25
US-08-605-284B-10
Sequence 10, Application US/08605284B
Patent No. 6060271
GENERAL INFORMATION:
APPLICANT: MALEWSKI, JOSE L.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TITLE OF INVENTION: VOLTAGE GATED SODIUM CHANNELS FROM
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: CLINTON SQUARE, P.O. BOX 1051
CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,284B
FILING DATE: 09-FEB-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/800 (CRF D-1705)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-605-284B-10

Query Match 57.1%; Score 16; DB 3; Length 310;
Best Local Similarity 100.0%; Pred. No. 8.2e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GIFFVSYIIISFLV 16
DB 1 GIFFVSYIIISFLV 16

Fri Jan 28 09:32:03 2005

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Search completed: January 27, 2005, 17:54:20
Job time : 23.5 secs